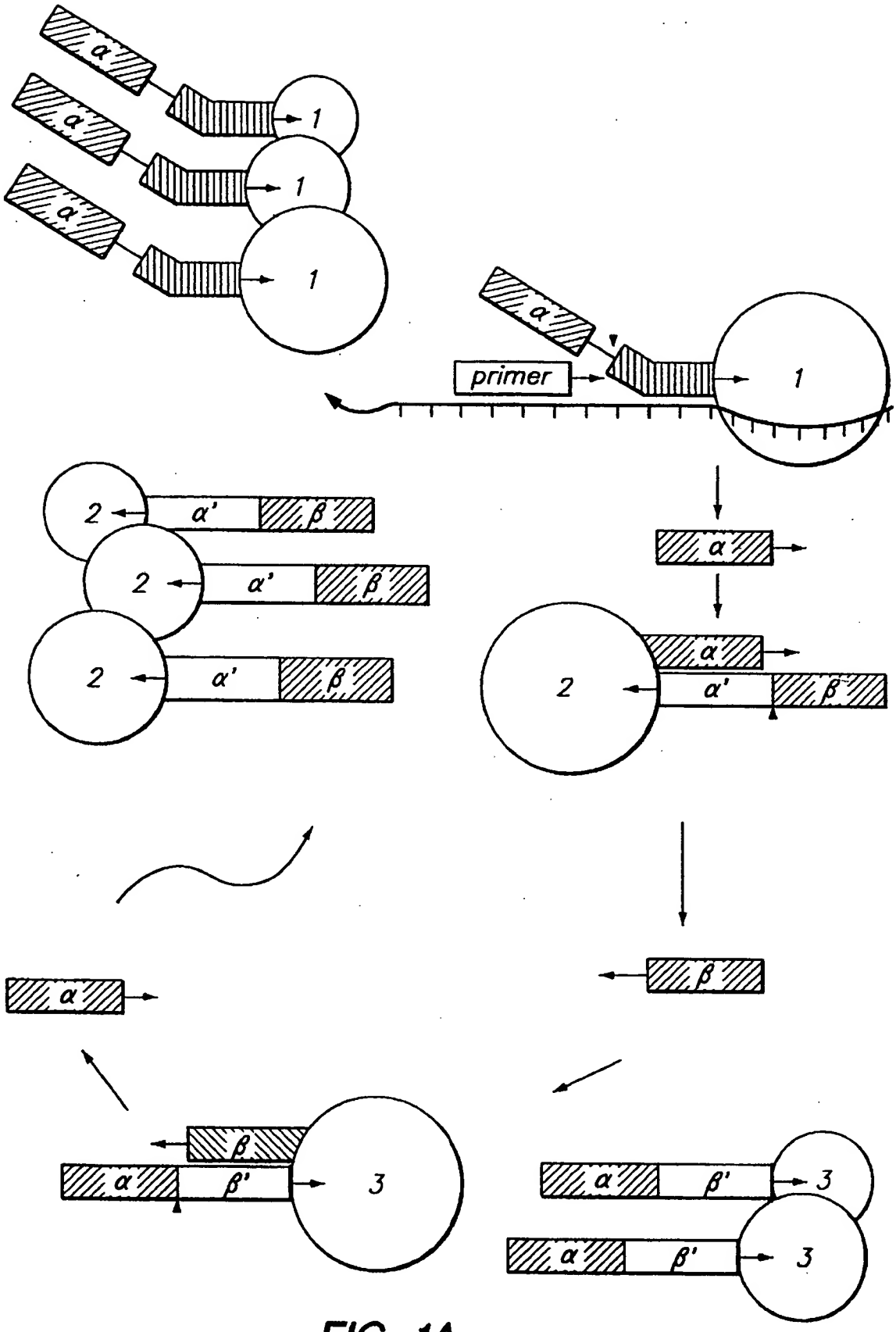


FIG. 1A

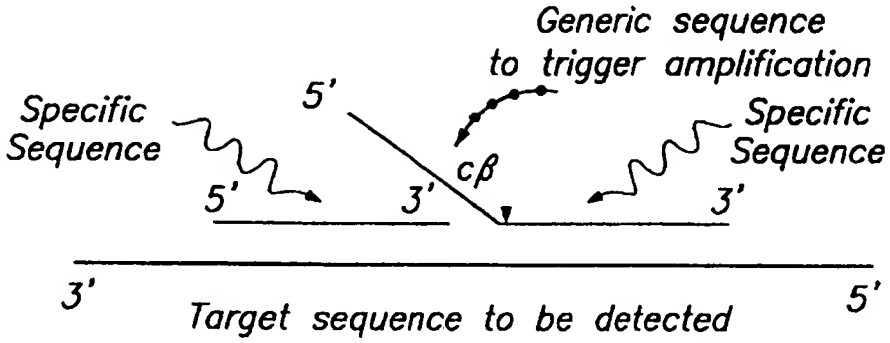


FIG. 1B PART ONE: TRIGGER REACTION

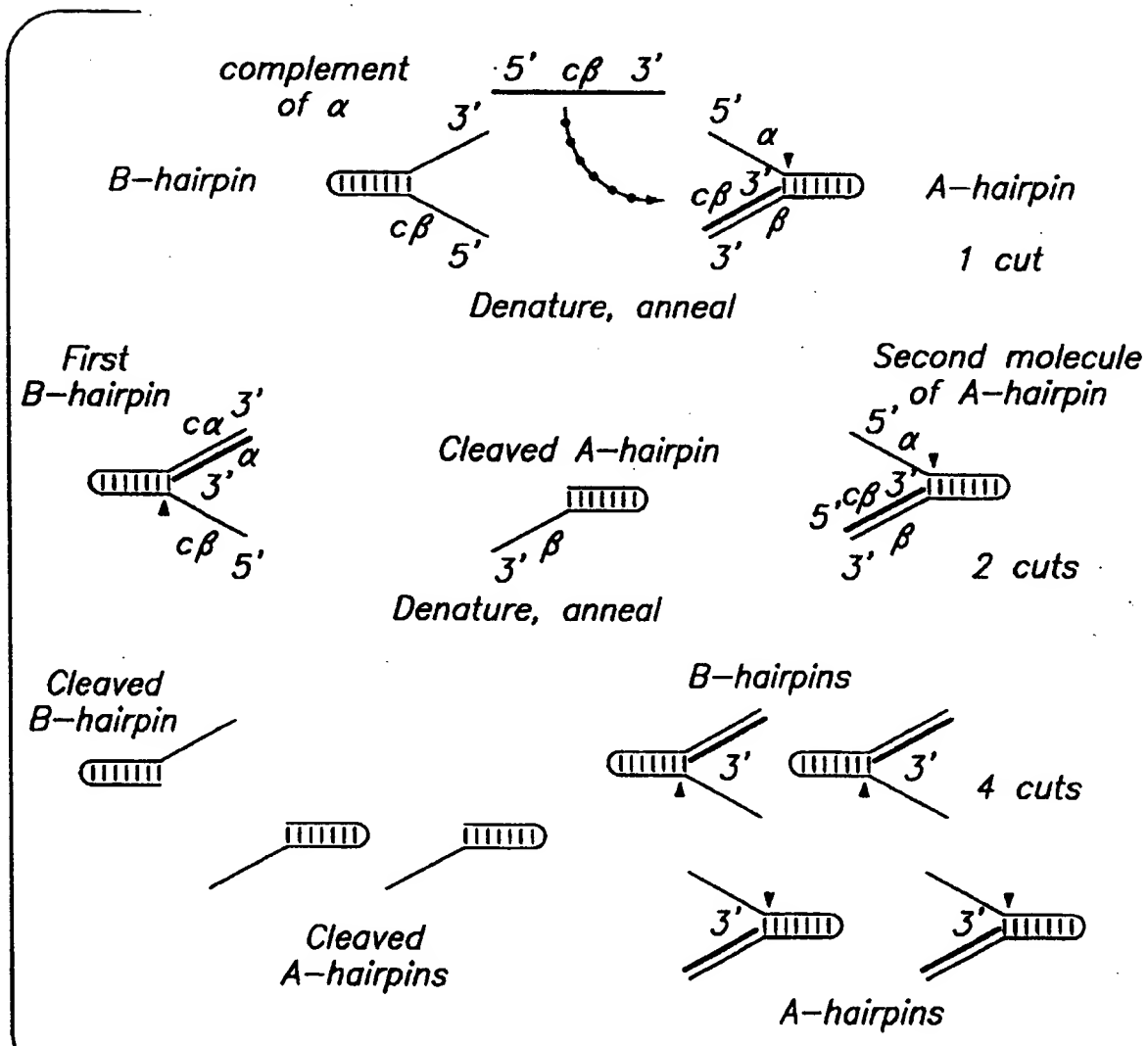


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

```
MAJORITY [SEQ ID NO:7] ATGXXGGCGATGCTTCCCCTCTTTGAGCCCAAAGGCCGGGTCCTCCTGGTGGACGGCCACCACCTGGCCT

DNAPTAQ  [SEQ ID NO:1] ...AG..G.....G.................G.....................................  70
DNAPTFL  [SEQ ID NO:2] .....................................C..G.....................................  67
DNAPTTH  [SEQ ID NO:3] ...GA..........G.......A.....................................  70

MAJORITY ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCAGCCGGGGCGAACCGGTGCAGGCGGTCTACGGCTT

DNAPTAQ  ..........CA.....................................G..G.....................  140
DNAPTFL  ............T.....C.....................C.......C..T.....................  137
DNAPTTH  .....................................G.....................................  140

MAJORITY CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGGCGGTGXTCGTGGTCTTTGACGCCAAG

DNAPTAQ  ........................C.....................A.....................  207
DNAPTFL  ......A.....................................GT..T.....................  204
DNAPTTH  .....................................T..AA...C..CT.....................  210

MAJORITY GCCCCCTCCTTCCGCCACGAGGCCTACGAGGCCTACAAGGCGGGCCGGGCCCCCACCCCGGAGGACTTTC

DNAPTAQ  ............................G..GG.....................G.....  277
DNAPTFL  .....................................................  274
DNAPTTH  ..........................................GA.....G.....C.....C.  280

MAJORITY CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGCGCGCCTCGAGGTCCCCGGCTA

DNAPTAQ  .....A.....................................G.....G.....  347
DNAPTFL  .........G.............T.............A..C....T...G..G.....T.....T  344
DNAPTTH  .....................................T..A.C.....................  350
```

FIG. 2B

```
MAJORITY [SEQ ID NO:7] CGAGGCGGACGACGTXGTGGCCACCCTGGCCAAGAAGGCGGAAAAGGAGGGGTACGAGGTGCGCATCCTC

DNAPTAQ  [SEQ ID NO:1] ..............C.......G.............................C........C.........  417
DNAPTFL  [SEQ ID NO:2] T.............G.................CG.....................................  414
DNAPTTH  [SEQ ID NO:3] ..............T..C.....................................................  420

MAJORITY ACCGCCGACCGCGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA

DNAPTAQ  .........AAA.....T.........................CA.............................  487
DNAPTFL  ..T.............................G..G.........A..........T...........G.  484
DNAPTTH  ........................A...G.C.........G.....................CC......  490

MAJORITY TCACCCCGGCGTGGCTTTGGGAGAAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC

DNAPTAQ  ..........C...........A.................C..C.......CC..............A.  557
DNAPTFL  ..................AC..............C.C.................................  554
DNAPTTH  .........A.........................C.....................T...C.....C.T  560

MAJORITY GGGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAAGACCGCCCXGAAGCTCCTCXAG

DNAPTAQ  C......GAG...........T.............................G..GAG......T..GG..  627
DNAPTFL  ............G..T...A.........G.........................A..G....A..CGC  624
DNAPTTH  ..................................................TC.........A..  630

MAJORITY GAGTGGGGGAGCCTGGAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC···CXTCCGGGAGAAGA

DNAPTAQ  ..................GC.....................C.............A.............  694
DNAPTFL  ........................T..C..C.........A..........T.····T.G.........C  691
DNAPTTH  ........A.....................................A.....A.AAAA.G.............  700
```

FIG. 2C

```
MAJORITY [SEQ ID NO:7] TCCAGGCCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCCAGGTGCGCACCGACCTGCCCCTGGA

DNAPTAQ  [SEQ ID NO:1] ...T.....C..T....A.....C..GG..A..... 764
DNAPTFL  [SEQ ID NO:2] .......GGG.....G.C....GCC..T...C..A....T.....A...T..... 761
DNAPTTH  [SEQ ID NO:3] ..A.....C....A.....C.G.....T.....C....G.....C..... 770

MAJORITY GGTGGACTTCGCCAAGXGGCGGGAGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT

DNAPTAQ  .....AA.....A.....T..... 834
DNAPTFL  .....GG.G.C.C..CACA...A...T.....T..GC....T...T.....C..T..... 831
DNAPTTH  .....C.....C..G.....C.....C 840

MAJORITY GGCAGCCTCCTCCACGAGTTCGGCCTCCTGGAGGGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCCCGC

DNAPTAQ  .....T.....AA..... 904
DNAPTFL  ..A.....G..G.....GGCA.....T. 901
DNAPTTH  .....C....GCCC..... 910

MAJORITY CGGAAGGGGCCTTCGTGGGCTTTGTCCTTTCCCGCCCCGAGCCCATGTGGGCCGAGCTTCTGGCCCTGGC

DNAPTAQ  .....G.....AAG.....T..... 974
DNAPTFL  .....T..TT.....TC.T.....T..... 971
DNAPTTH  .....C.....C.....G.....AAA..... 980

MAJORITY CGCCGCCAGGGAGGGCCGGGTCCACCGGGCACCAGACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG

DNAPTAQ  .....G.....C..C..G..T.A..AA.C...C.....G.....C. 1044
DNAPTFL  T.GG..GT.....G..CC....T.....A.....C...G.....G.....T....G.... 1041
DNAPTTH  ....TG.....C.....G.....G.....GGC...G..A.A.....C.....C 1050
```

FIG. 2D

```
MAJORITY [SEQ ID NO:7]  CGGGGXCTCCTCGCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCGGGGACG

DNAPTAQ  [SEQ ID NO:1]  .....G..T........A......AG....C.............A.....T.G....CC......C....  1114
DNAPTFL  [SEQ ID NO:2]  .....AA....G..............G............C..........G......T.C..A.A.....  1111
DNAPTTH  [SEQ ID NO:3]  .....C.................C.....C......TC.........G..A......G............  1120

MAJORITY                ACCCCATGGTCGTCGGCTACCTCCTGGACCCGTCGAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGG

DNAPTAQ                 ...............................T......................................  1184
DNAPTFL                 .............G........T.......................T.................T.....  1181
DNAPTTH                 ..........................................................G...........  1190

MAJORITY                GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCGTCGTXTCGGAGAGGCTCTTCCXGAACCTXXXGGAG

DNAPTAQ                 C.................G...............GC...T...............GCC.....GTG..G.  1254
DNAPTFL                 ..................T.........A..........GG.....C.C.......A..C...AAA....  1251
DNAPTTH                 ..................C..C.CCC.C...........C..G.........CAT.G......CCTTA..  1260

MAJORITY                CGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCTGG

DNAPTAQ                 A.G..................................G...........G..........GCT.......  1324
DNAPTFL                 ......A....A..A..AC.C..G............G................G...........GT...  1321
DNAPTTH                 .....C.............A............C.....C........A........C.............  1330

MAJORITY                CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

DNAPTAQ                 ......................G..C..............T...AG....T.G..............C..  1394
DNAPTFL                 ...GG.................C.............................C.............A..C  1391
DNAPTTH                 ................C.....A....................T........T.........C.T.....  1400
```

FIG. 2E

```
MAJORITY [SEQ ID NO:7] GGAGATCCGCCGCCTCGAGGAGGAGGTCTTCGGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC

DNAPTAQ  [SEQ ID NO:1] .......GC..........CC.....................................................  1464
DNAPTFL  [SEQ ID NO:2] ....G.G....AG..G.....................................................C...  1461
DNAPTTH  [SEQ ID NO:3] ..................................T....G.....................................  1470

MAJORITY CAGCTGGAAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC

DNAPTAQ  ..............C..............A.....................................C.......  1534
DNAPTFL  .......GC.....................G..C..G..T.....................G..G..A.  1531
DNAPTTH  ..............................TA..........T.G..G......C.A.....A.......  1540

MAJORITY GCTCCACCAGCGCCGCCGTGCTGGAGGCCCTXCGXGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQ  ....................C..........C..C.....................................  1604
DNAPTFL  .............T.....................G..A.....................CCGC.........  1601
DNAPTTH  ................G.............A..G.....................................C...C.  1610

MAJORITY CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCCTGCCXGXCCTCGTCCACCCCAGGACGGGC

DNAPTAQ  ..................G....G.........T......T....G.A....A.....................  1674
DNAPTFL  ..................................A..........C.C...G.........A...C...  1671
DNAPTTH  ..............................G.G.......C..AAG............G.........  1680

MAJORITY CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC

DNAPTAQ  ..................................................A..........T........C.  1744
DNAPTFL  ..G.............................C..............TCC.....................  1741
DNAPTTH  ..................................................G.....................  1750
```

FIG. 2F

```
MAJORITY [SEQ ID NO:7] AGAACATCCCCGTCCGCACCCCXCTGGGCCAGAGGATCCGCCGGGCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAQ  [SEQ ID NO:1] .....G..T..G.....A.C.....G...C.  1814
DNAPTFL  [SEQ ID NO:2] .....G.....T.....C.C.....A.....C.....  1811
DNAPTTH  [SEQ ID NO:3] .....CT.....C...T....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ  A.....A....G.....C..... 1884
DNAPTFL  .C.....T.T.....C.....T....T..... 1881
DNAPTTH  .....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGGACATCCACACCCAGACCGCCAGCTGGATGTTCGGCGTCCCCCCGG

DNAPTAQ  .....C.....GG.....G.. 1954
DNAPTFL  .....T.....TT....C. 1951
DNAPTTH  ...A.....A.....A..... 1960

MAJORITY AGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCCGC

DNAPTAQ  .....G.. 2024
DNAPTFL  .A.GG..A....T.....G..... 2021
DNAPTTH  .....GG.G.....C..... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCATCCCCTACGAGGAGGCGGTGGCCTTCATTGAGCGCTACTTCCAG

DNAPTAQ  .....A.....T.....CCA.....T... 2094
DNAPTFL  .....GG.....T..... 2091
DNAPTTH  ...TA.G.....T..A.....A 2100
```

FIG. 2G

```
MAJORITY [SEQ ID NO:7]  AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGA

DNAPTAQ  [SEQ ID NO:1]  ......................................................................  2164
DNAPTFL  [SEQ ID NO:2]  ....A.........................GG......C.........C.CC..........T.......  2161
DNAPTTH  [SEQ ID NO:3]  ..........................A..A.................G....A......C........A.  2170

        MAJORITY        CCCTCTTCGGCCGCCGGCGCTACGTGCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA

        DNAPTAQ         ................C...........A.....AG.G.............................C..  2234
        DNAPTFL         ......................T...................................C...........  2231
        DNAPTTH         ..........AA.AA........................................CA.......C.....  2240

        MAJORITY        GCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC

        DNAPTAQ         .........................................................T............  2304
        DNAPTFL         .....................G..........................................CG...T  2301
        DNAPTTH         ......................................................C...............  2310

        MAJORITY        TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCGTXCAGGTCCACGACGAGCTGGTCCTCGAGGCCC

        DNAPTAQ         ......A....GG.........................T...............................  2374
        DNAPTFL         ...........T......C.......G........TT.G.....G.........................  2371
        DNAPTTH         ........C..C.G...G.........C.C........C.................CC....G.......  2380

        MAJORITY        CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAGGAGGTCATGGAGGGGGTCTATCCCCTGGCCGT

        DNAPTAQ         .A......A.........CC......CGGC.........................G..............  2444
        DNAPTFL         ....G..C.........AG...A..................................GG......CAG..  2441
        DNAPTTH         ..C...C......C....A......G................C.......AA..C.........C.....  2450
```

FIG. 2H

```
MAJORITY [SEQ ID NO:7] GCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG

DNAPTAQ  [SEQ ID NO:1] .....A.....GA 2499
DNAPTFL  [SEQ ID NO:2] .....CC..... 2496
DNAPTTH  [SEQ ID NO:3] .....T.....GT... 2505
```

FIG. 3A

```
MAJORITY [SEQ ID NO:8]  MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG-DAVXVVFDAK

TAQ PRO  [SEQ ID NO:4] .RG........................H....................................I.....  69
TFL PRO  [SEQ ID NO:5] ..............................................................V.V.....  68
TTH PRO  [SEQ ID NO:6] .E..........................................................YK..F.....  70

MAJORITY                APSFRHEAYEAYKAGRAPTPEDFPRQLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL

TAQ PRO                 .........GG............................A...............S..............  139
TFL PRO                 .......................................V.......F...........R..........  138
TTH PRO                 ......................................FT..............................  140

MAJORITY                TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSDNLPGVKGIGEKTAXKLLX

TAQ PRO                 ...K..........H......................D..A.....T..E................R..E  209
TFL PRO                 ...........E...I.............Y................A......I...........QR.IR  208
TTH PRO                 .........V...V.......H....E...............F...V...................L..K  210

MAJORITY                EWGSLENLLKNLDRVKP-XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRAFLERLEF

TAQ PRO                 ......A.......L...AI....L...D..K..WD.AK............K.......R..........  278
TFL PRO                 ........FQH..Q....SL...LQ.G..A.A..RK..QH..........GR..T..NL...........  277
TTH PRO                 .................ENV....K..L...R..LE..R..........L.QG.................  280

MAJORITY                GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAELLALAAARXGRVHRAXDPLXGLRDLKEV

TAQ PRO                 ...........S.......................K.....D........G......PE.YKA......A  348
TFL PRO                 ...........G...A............L..SF..............G.WE..L...Q...R......G.  347
TTH PRO                 ...........A.AP............................K....C.D......A...A..K.....  350
```

FIG. 3B

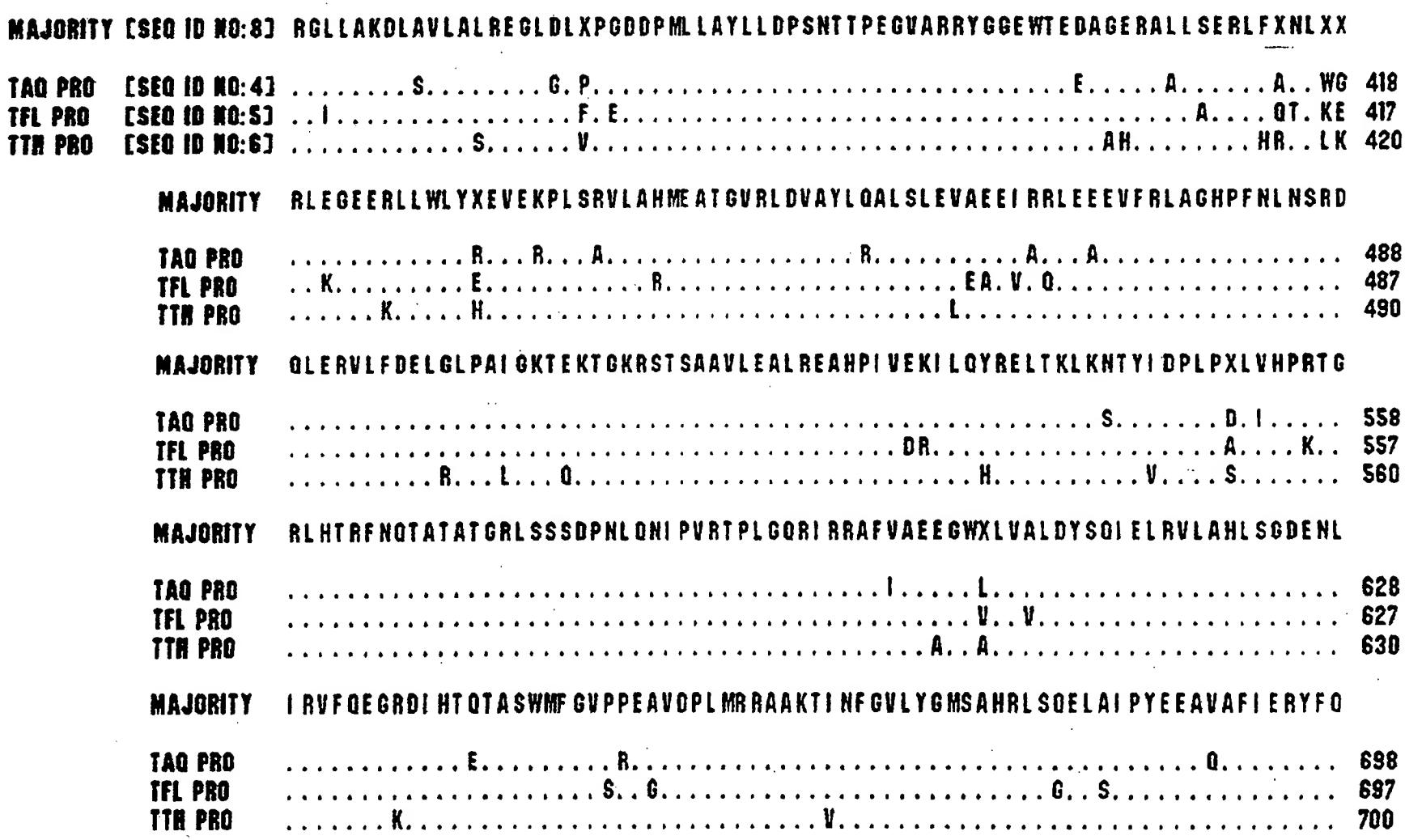

MAJORITY [SEQ ID NO:8] RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEDAGERALLSERLFXNLXX
TAQ PRO [SEQ ID NO:4] .....S.....G.P.....E.....A.....A..WG 418
TFL PRO [SEQ ID NO:5] ..I.....F.E.....A....QT.KE 417
TTH PRO [SEQ ID NO:6] .....S.....V.....AH.....HR..LK 420
MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVFRLAGHPFNLNSRD
TAQ PRO .....R...R...A.....R.....A...A..... 488
TFL PRO ..K.....E.....R.....EA.V.Q..... 487
TTH PRO .....K.....H.....L..... 490
MAJORITY QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRTG
TAQ PRO .....S.....D.I..... 558
TFL PRO .....DR.....A....K.. 557
TTH PRO .....R...L...Q.....H.....V....S..... 560
MAJORITY RLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL
TAQ PRO .....I.....L..... 628
TFL PRO .....V..V..... 627
TTH PRO .....A..A..... 630
MAJORITY IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAVAFIERYFQ
TAQ PRO .....E.....R.....Q..... 698
TFL PRO .....S..G.....G..S..... 697
TTH PRO .....K.....V..... 700

FIG. 3C

```
MAJORITY [SEQ ID NO:8] SFPKVRAWIEKTLEEGRRRGYVETLFGRRRYVPDLNARVKSVREAAERMAFNMPVQGTAADLMKLAMVKL

TAQ PRO  [SEQ ID NO:4] ..........................................E.....................................  768
TFL PRO  [SEQ ID NO:5] .Y.......G.....................................................................R.  767
TTH PRO  [SEQ ID NO:6] ................K.....................................................................  770

MAJORITY FPRLXEMGARMLLQVHDELVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PRO  ....E.....................E...A..R.....................I.........  833
TFL PRO  ....Q.L...................D...R.............W..Q.......L.........  831
TTH PRO  ....R.............L....QA...E.......A..KA............M........G  835
```

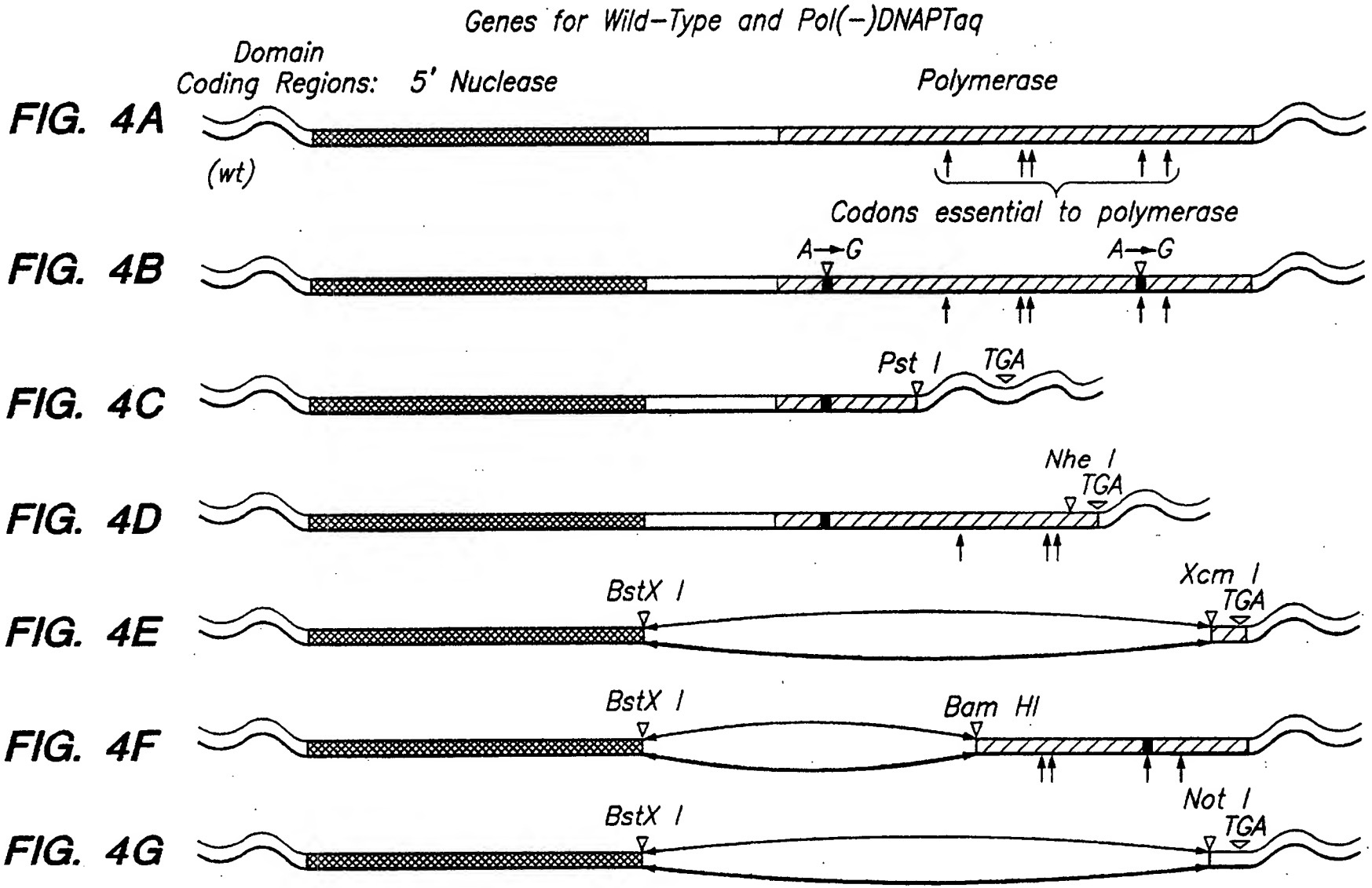


FIG. 4A

FIG. 4B

FIG. 4C

FIG. 4D

FIG. 4E

FIG. 4F

FIG. 4G

Genes for Wild-Type and Pol(-) DNAPTfl

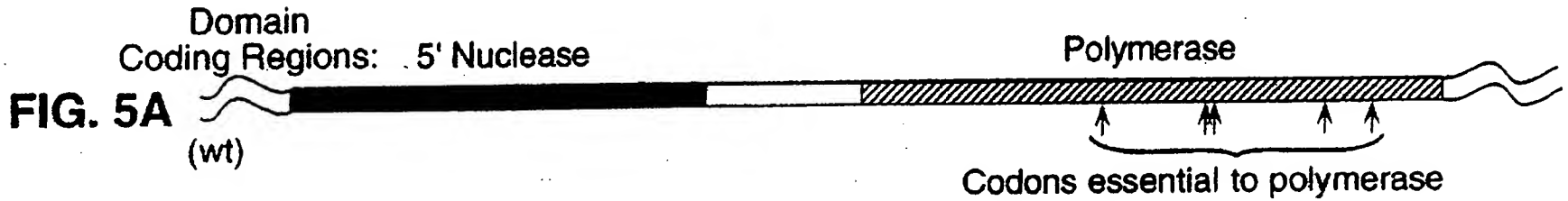


FIG. 5A

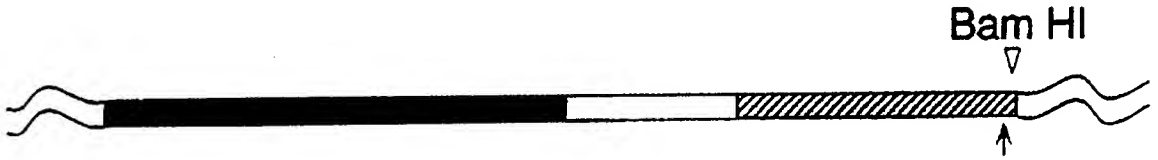


FIG. 5B

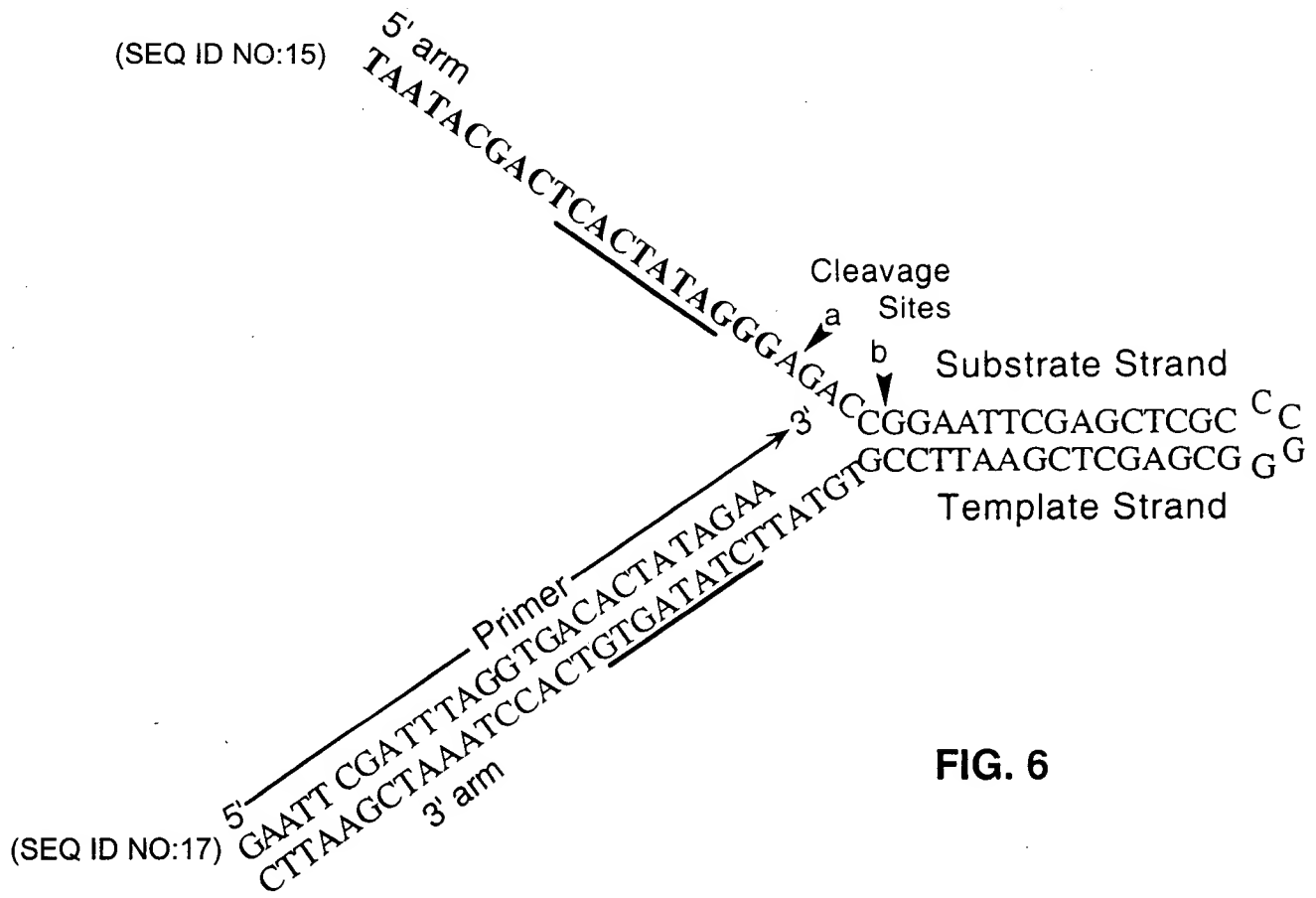

(SEQ ID NO:15)
5' arm
TAATACGACTCACTATAGGGAGAC
Cleavage
Sites
a
b
Substrate Strand
3'
CGGAATTCGAGCTCGC C C
GCCTTAAGCTCGAGCG G G
Template Strand
Primer
5'
GAATT CGATTTAGGTGACACTATAGAA
CTTAAGCTAAATCCACTGTGATATCTTATGT
3' arm
(SEQ ID NO:17)

FIG. 6

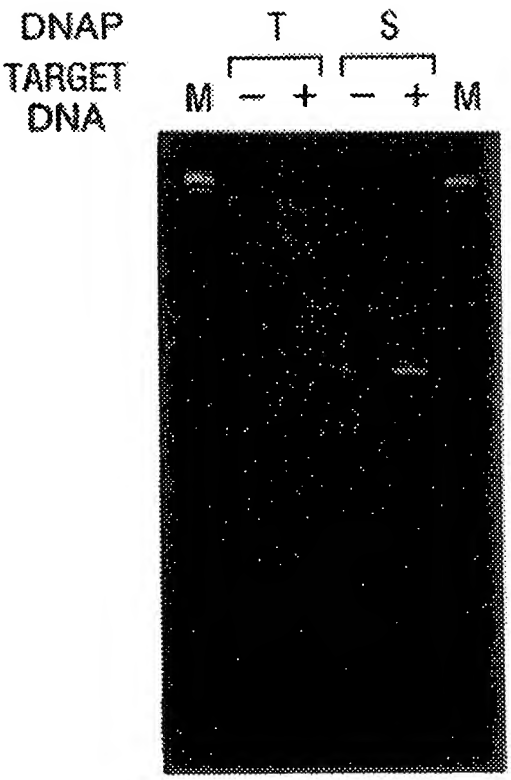


FIG. 7

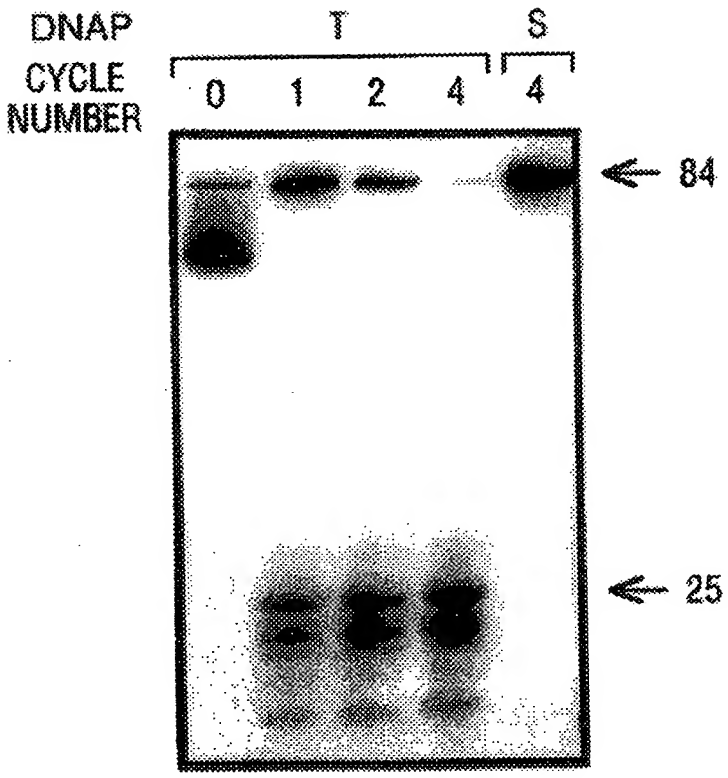


FIG. 8

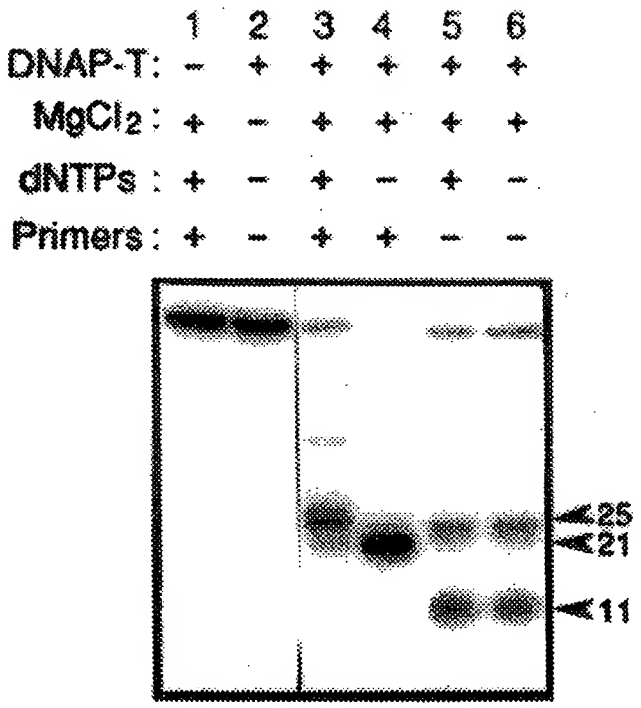


FIG. 9A

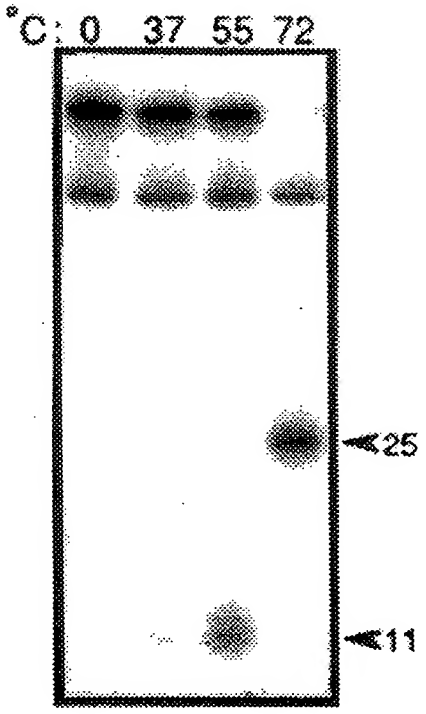


FIG. 9B

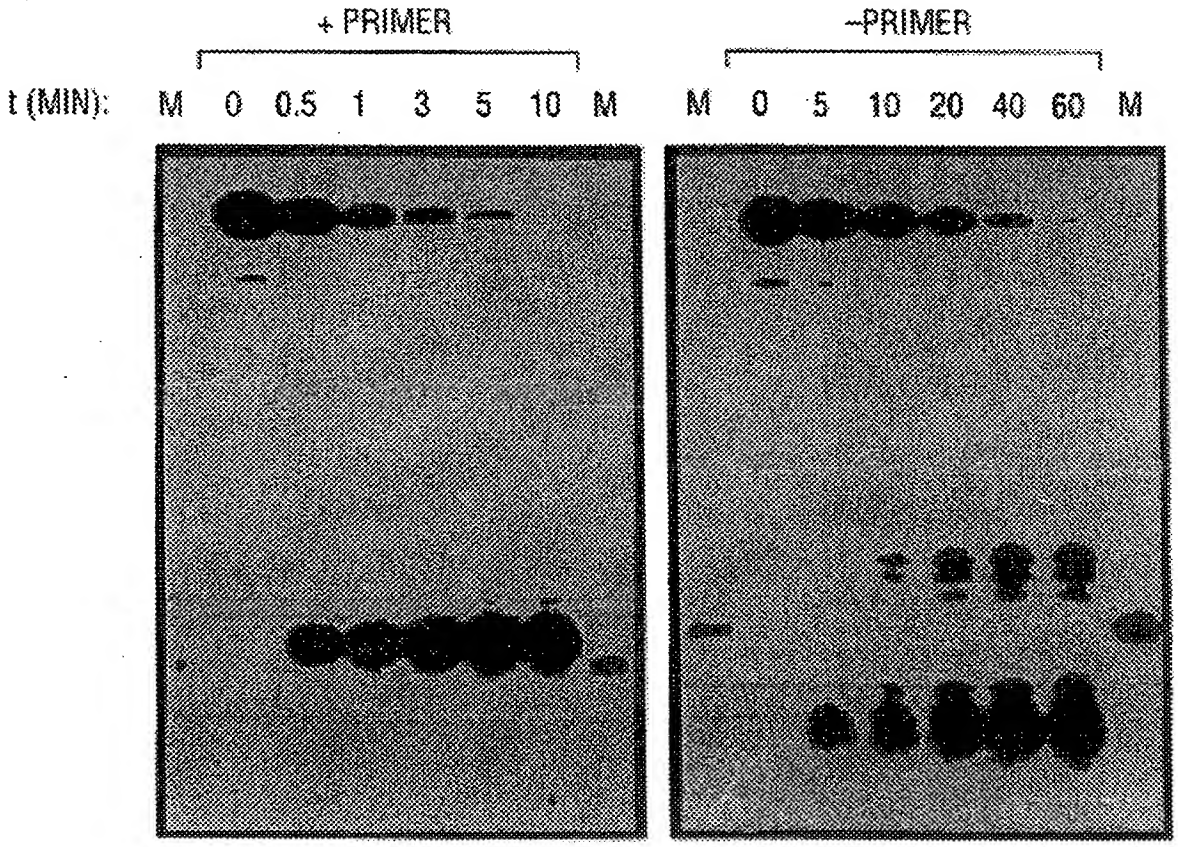


FIG. 10A

FIG. 10B

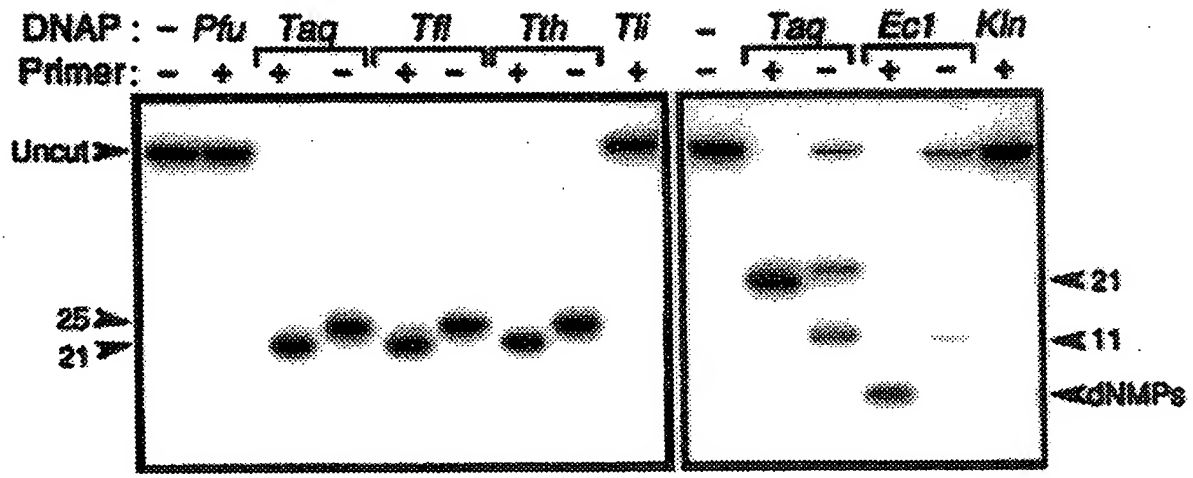
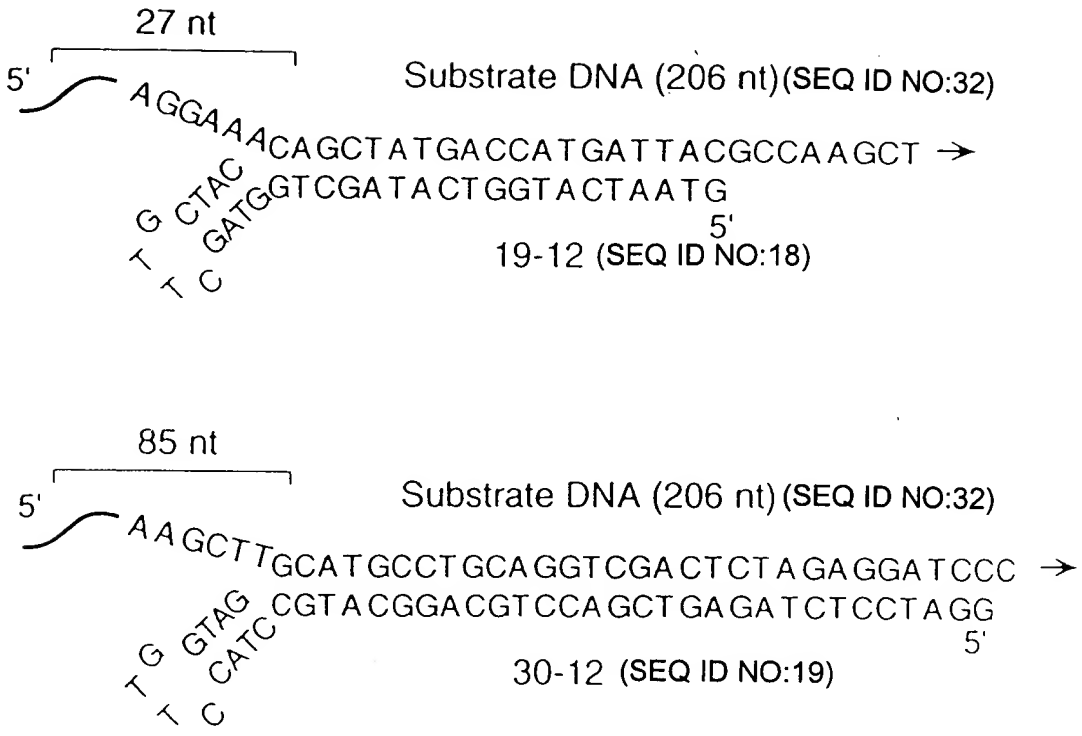


FIG. 11A

FIG. 11B

FIG. 12A


27 nt
5'
Substrate DNA (206 nt) (SEQ ID NO:32)
AGGAAACAGCTATGACCATGATTACGCCAAGCT →
TG CTAC
T GATGGTCGATACTGGTACTAATG
T C
5'
19-12 (SEQ ID NO:18)
85 nt
5'
Substrate DNA (206 nt) (SEQ ID NO:32)
AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCC →
TG GTAG CGTACGGACGTCCAGCTGAGATCTCCTAGG
T CATC
5'
30-12 (SEQ ID NO:19)

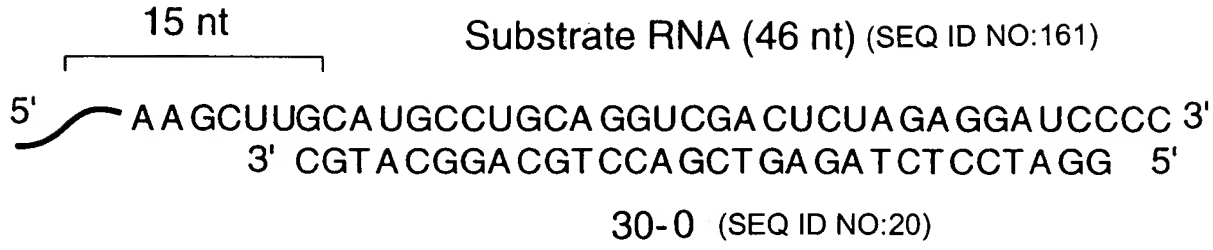

15 nt
Substrate RNA (46 nt) (SEQ ID NO:161)
5'
A A GCUUGCA UGCCUGCA GGUCGA CUCUA GA GGA UCCCC 3'
3' CGT A CGGA CGT CCA GCT GA GA T CT CCT A GG 5'
30-0 (SEQ ID NO:20)

FIG. 13A

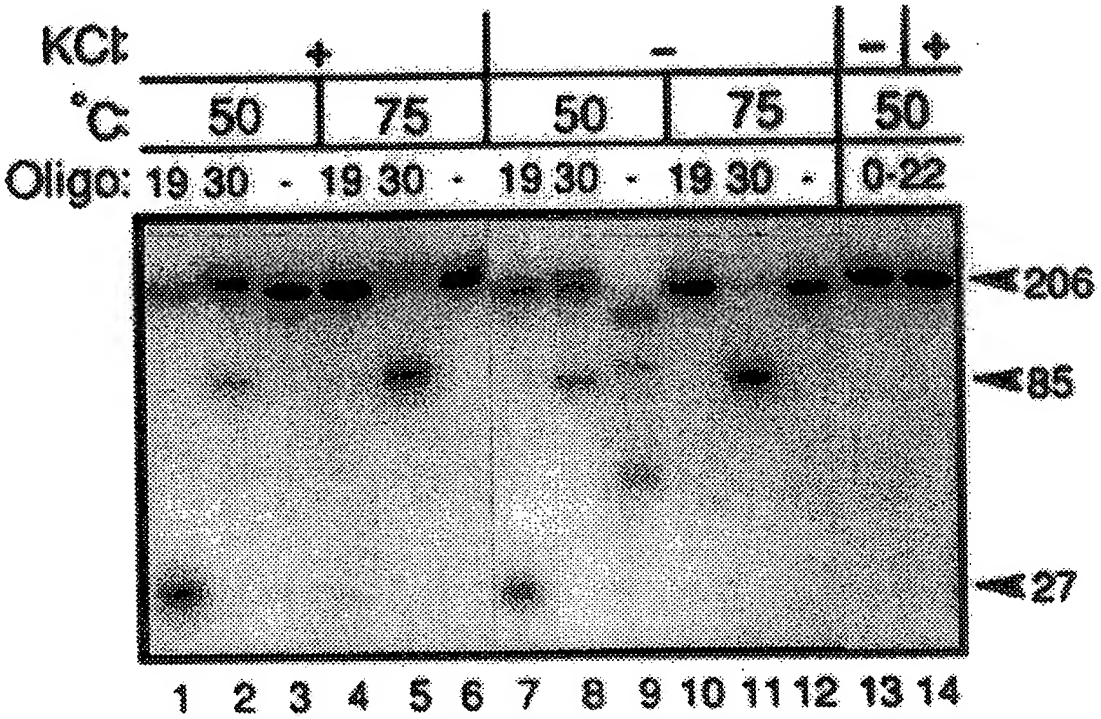


FIG. 12B

FIG. 13B

(SEQ ID NO:162)

-35 -10 RBS

TTGACAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCG

MetAsnSer...

ATGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC

EcoRI SstI KpnI SmaI BamHI XbaI SalI PstI SphI HindIII

FIG. 14B

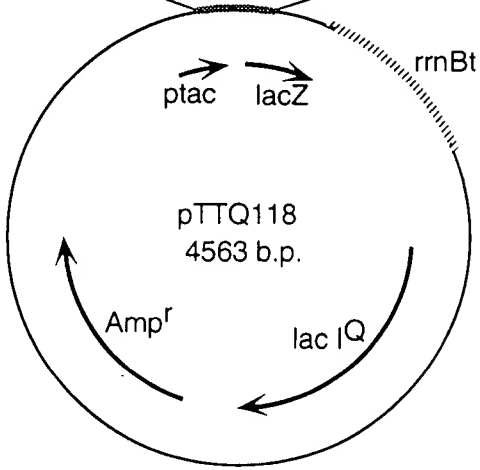


FIG. 14A

RBS: Ribosome binding site
ptac: Synthetic tac promoter
lac I^Q: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rrnBt: E. coli rrnB transcription terminator

FIG. 14C

(SEQ ID NO:163)

AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTT

Bgl II — T7 Promoter — XbaI

MetAlaSer...

AACTTTAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCGGATCCGGCT

RBS — NdeI — BamHI

FIG. 15B

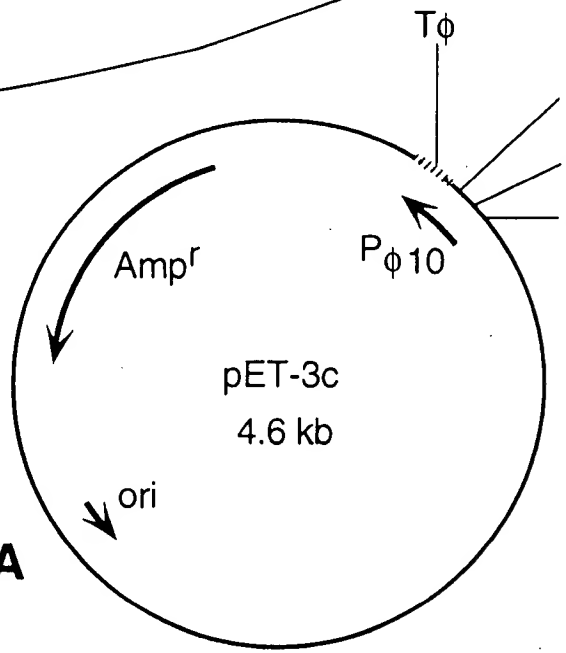


FIG. 15A

$P_{\phi 10}$: Bacteriophage T7 ϕ10 promoter

RBS: Ribosome binding site

Tϕ: T7 ϕ Terminator

FIG. 15C

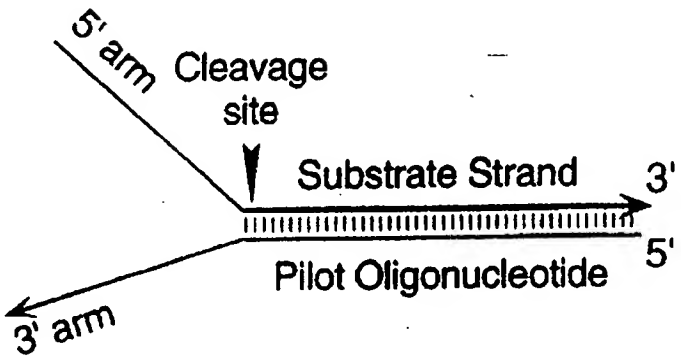


FIG. 16A

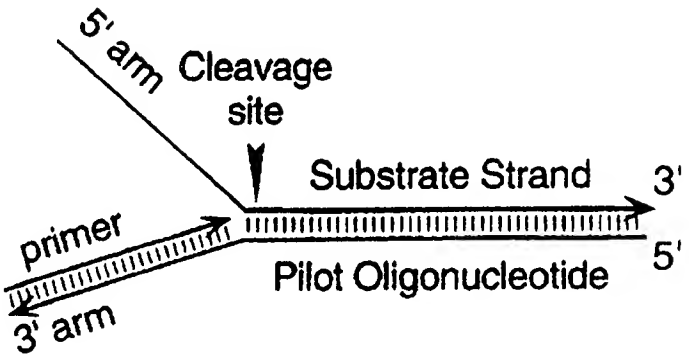


FIG. 16B

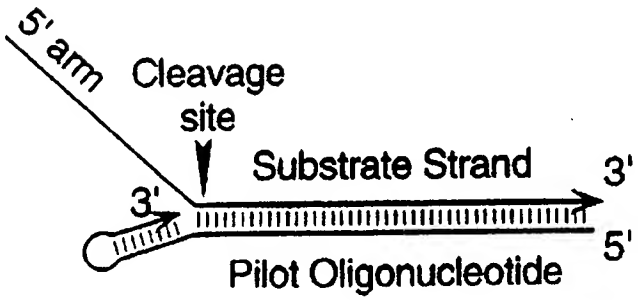


FIG. 16C

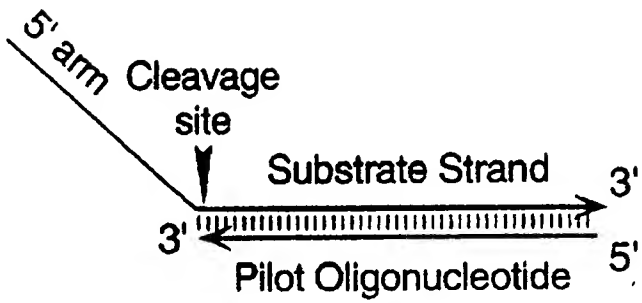


FIG. 16D

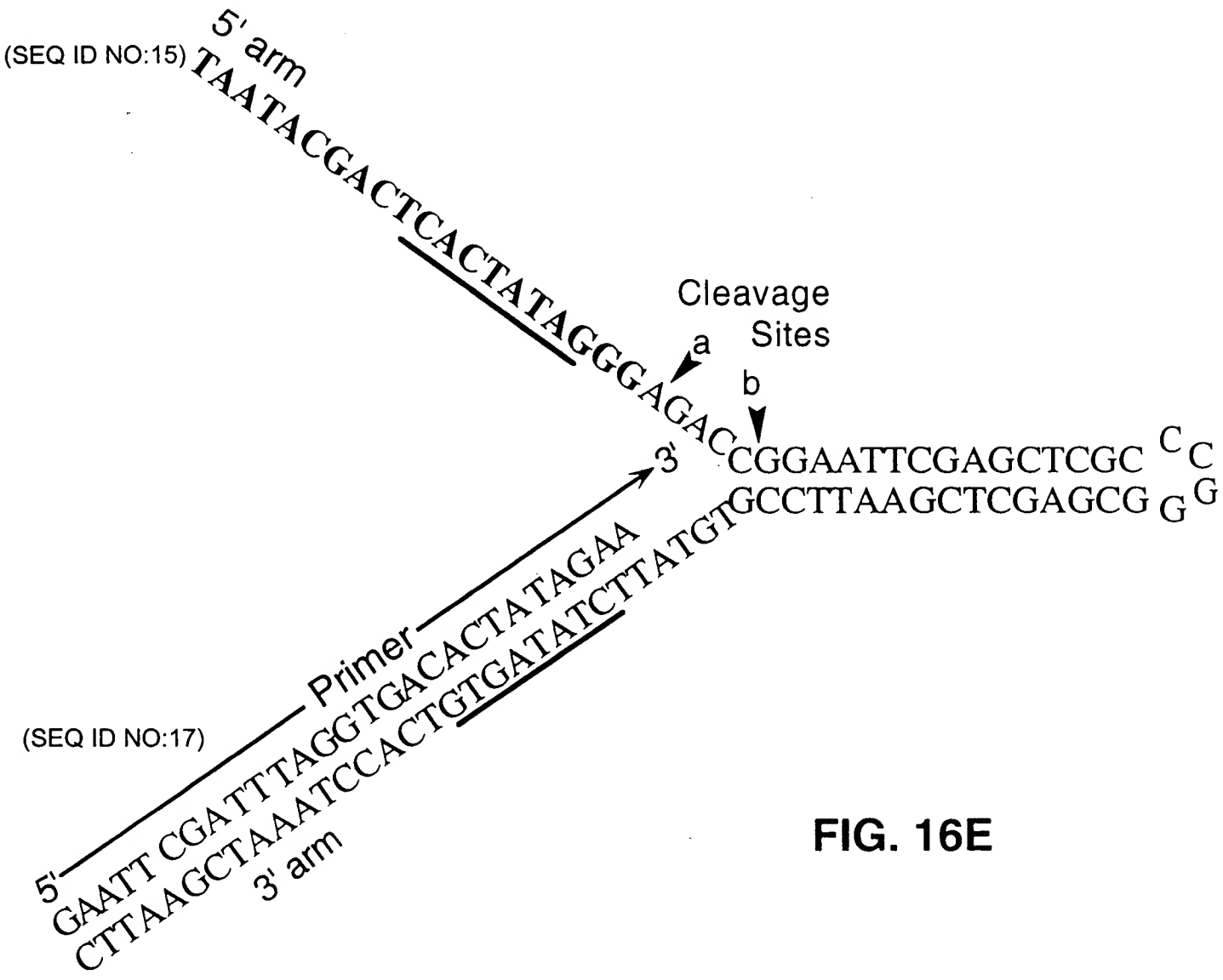

(SEQ ID NO:15)
5' arm
TAATACGACTCACTATAGGGAGACC
Cleavage
Sites
a
b
3'
CGGAATTCGAGCTCGC C C
GCCTTAAGCTCGAGCG G G
Primer
(SEQ ID NO:17)
5'
GAATT CGATTTAGGTGACACTATAGAA
CTTAAGCTAAATCCACTGTGATATCTTATGT
3' arm

FIG. 16E

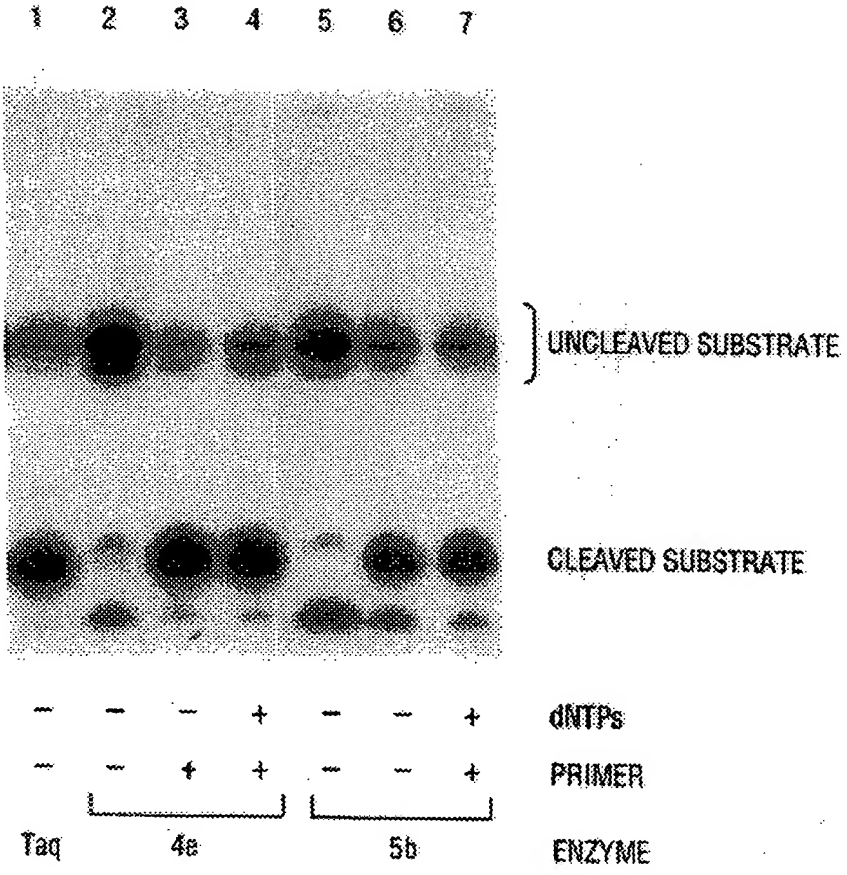

1 2 3 4 5 6 7
UNCLEAVED SUBSTRATE
CLEAVED SUBSTRATE
– – – + – – + dNTPs
– – + + – – + PRIMER
Taq 4e 5b ENZYME

FIG. 17

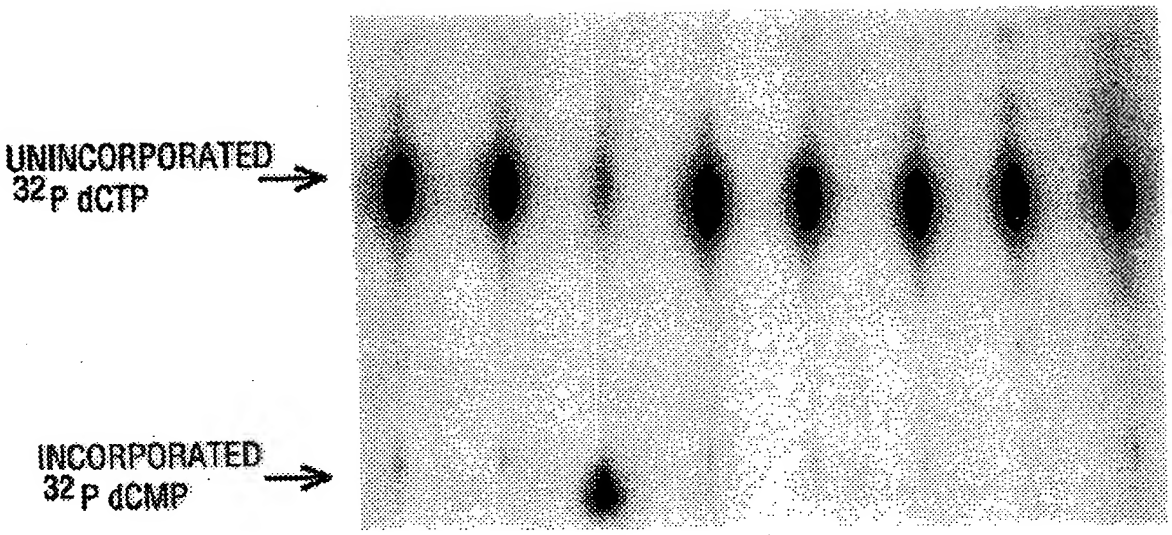

UNINCORPORATED
32P dCTP
INCORPORATED
32P dCMP
ENZYME Taq – Taq 4b 4c 4d 4e 4f
PRIMED M13 – + + + + + + +

FIG. 18

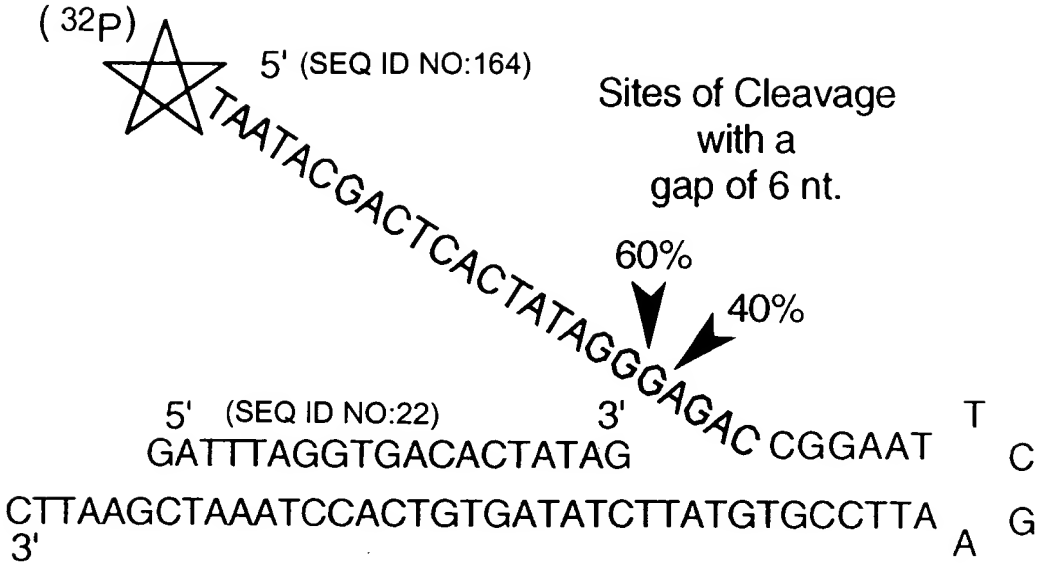

(32P)
5' (SEQ ID NO:164)
TAATACGACTCACTATAGGGAGAC
Sites of Cleavage
with a
gap of 6 nt.
60%
40%
5' (SEQ ID NO:22)
3'
GATTTAGGTGACACTATAG
CGGAAT
T
C
CTTAAGCTAAATCCACTGTGATATCTTATGTGCCTTA
A
G
3'

FIG. 19A

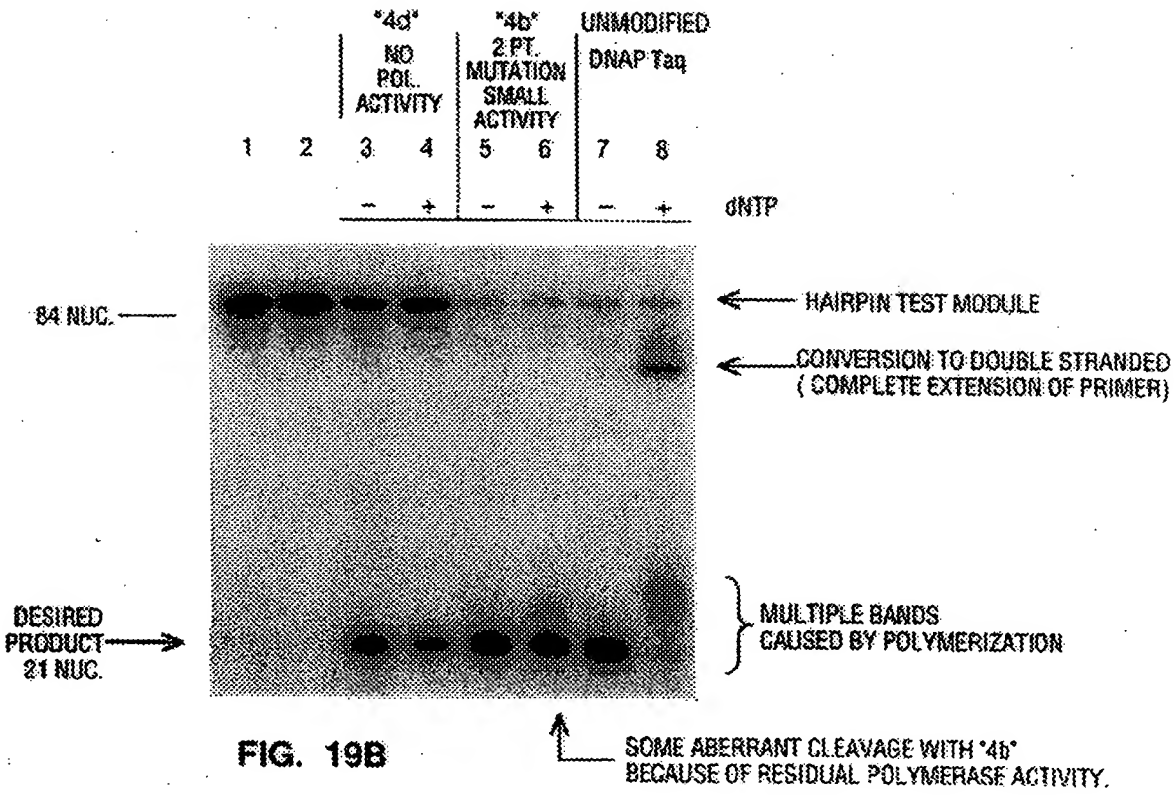

"4d"
NO POL. ACTIVITY
"4b"
2 PT. MUTATION SMALL ACTIVITY
UNMODIFIED
DNAP Taq
1 2 3 4 5 6 7 8
- + - + - +
dNTP
84 NUC.
HAIRPIN TEST MODULE
CONVERSION TO DOUBLE STRANDED
(COMPLETE EXTENSION OF PRIMER)
DESIRED PRODUCT
21 NUC.
MULTIPLE BANDS
CAUSED BY POLYMERIZATION
SOME ABERRANT CLEAVAGE WITH "4b"
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

FIG. 19B

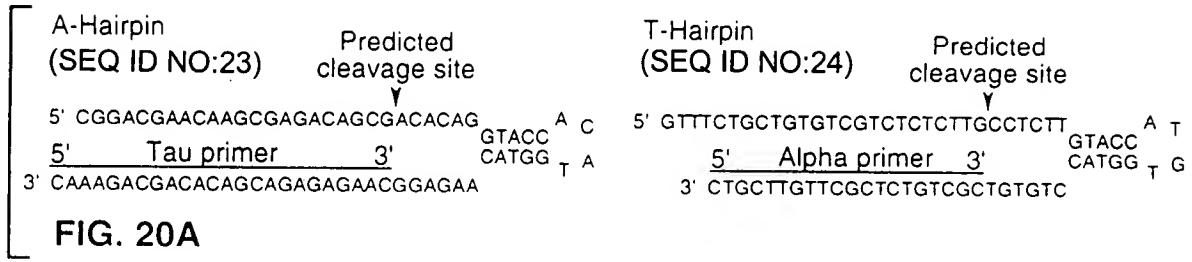


FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)

5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

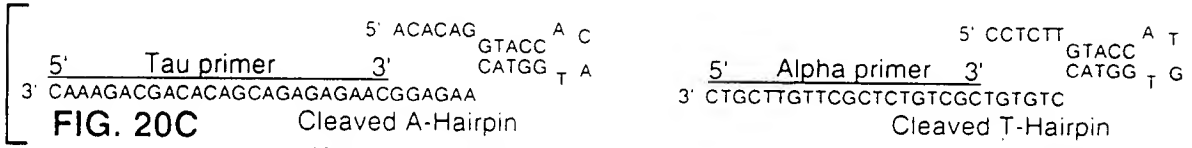


FIG. 20C

Cleaved A-Hairpin
(SEQ ID NO:28)

Cleaved T-Hairpin
(SEQ ID NO:27)

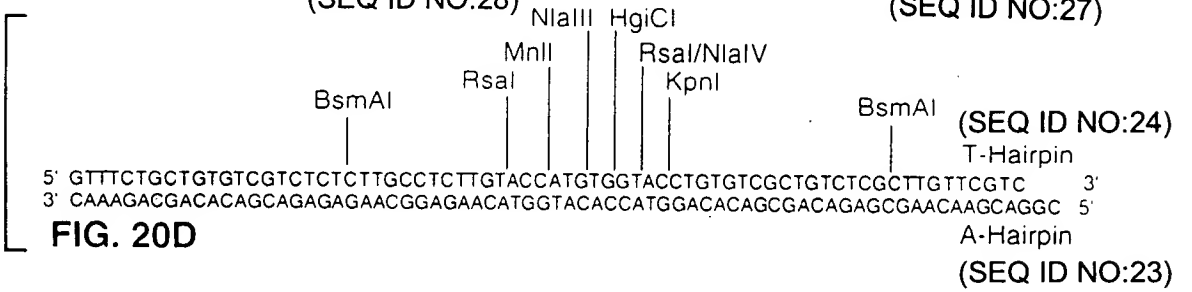


FIG. 20D

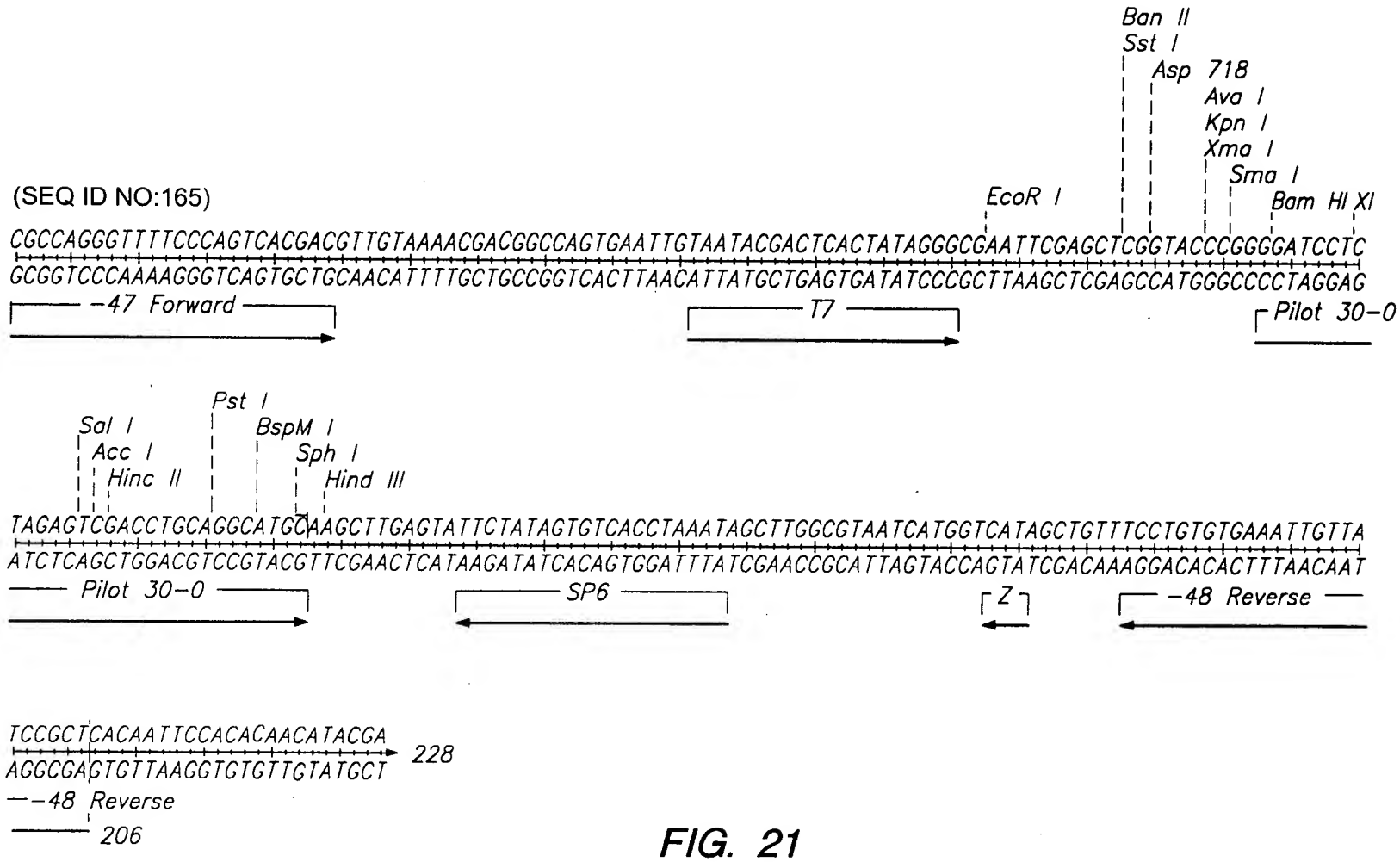

Ban II
Sst I
Asp 718
Ava I
Kpn I
Xma I
Sma I
Bam HI XI
EcoR I
(SEQ ID NO:165)
CGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTCGAGCTCGGTACCCGGGGATCCTC
GCGGTCCCAAAAGGGTCAGTGCTGCAACATTTTGCTGCCGGTCACTTAACATTATGCTGAGTGATATCCCGCTTAAGCTCGAGCCATGGGCCCCTAGGAG
-47 Forward
T7
Pilot 30-0
Pst I
Sal I
BspM I
Acc I
Sph I
Hinc II
Hind III
TAGAGTCGACCTGCAGGCATGCAAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA
ATCTCAGCTGGACGTCCGTACGTTCGAACTCATAAGATATCACAGTGGATTTATCGAACCGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAAT
Pilot 30-0
SP6
Z
-48 Reverse
TCCGCTCACAATTCCACACAACATACGA
AGGCGAGTGTTAAGGTGTGTTGTATGCT
228
--48 Reverse
206

FIG. 21

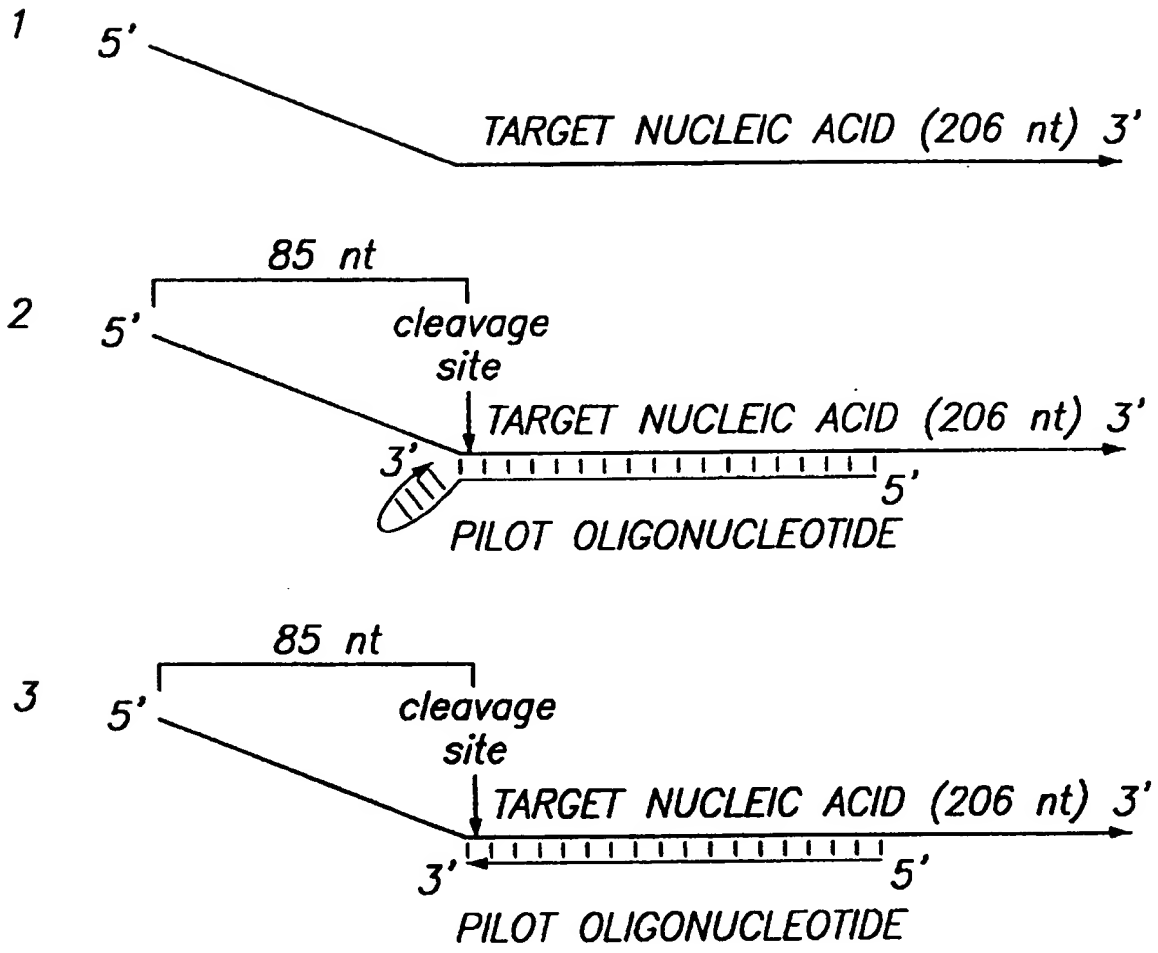

1
5'
TARGET NUCLEIC ACID (206 nt) 3'
85 nt
2
5'
cleavage
site
TARGET NUCLEIC ACID (206 nt) 3'
3'
5'
PILOT OLIGONUCLEOTIDE
85 nt
3
5'
cleavage
site
TARGET NUCLEIC ACID (206 nt) 3'
3'
5'
PILOT OLIGONUCLEOTIDE

FIG. 22A

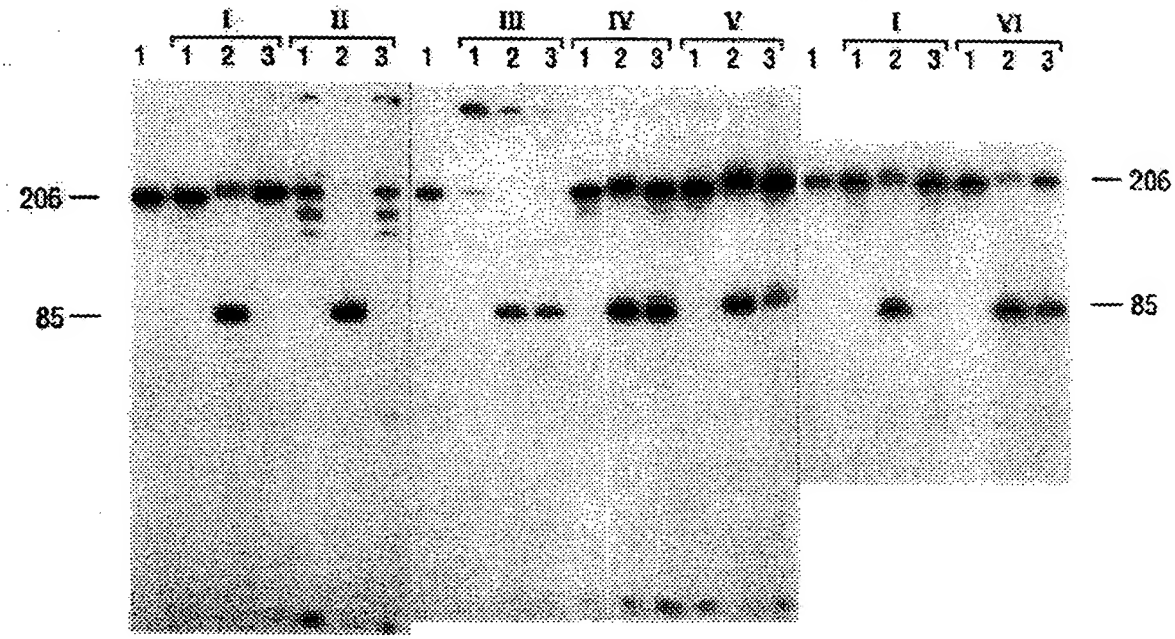


FIG. 22B

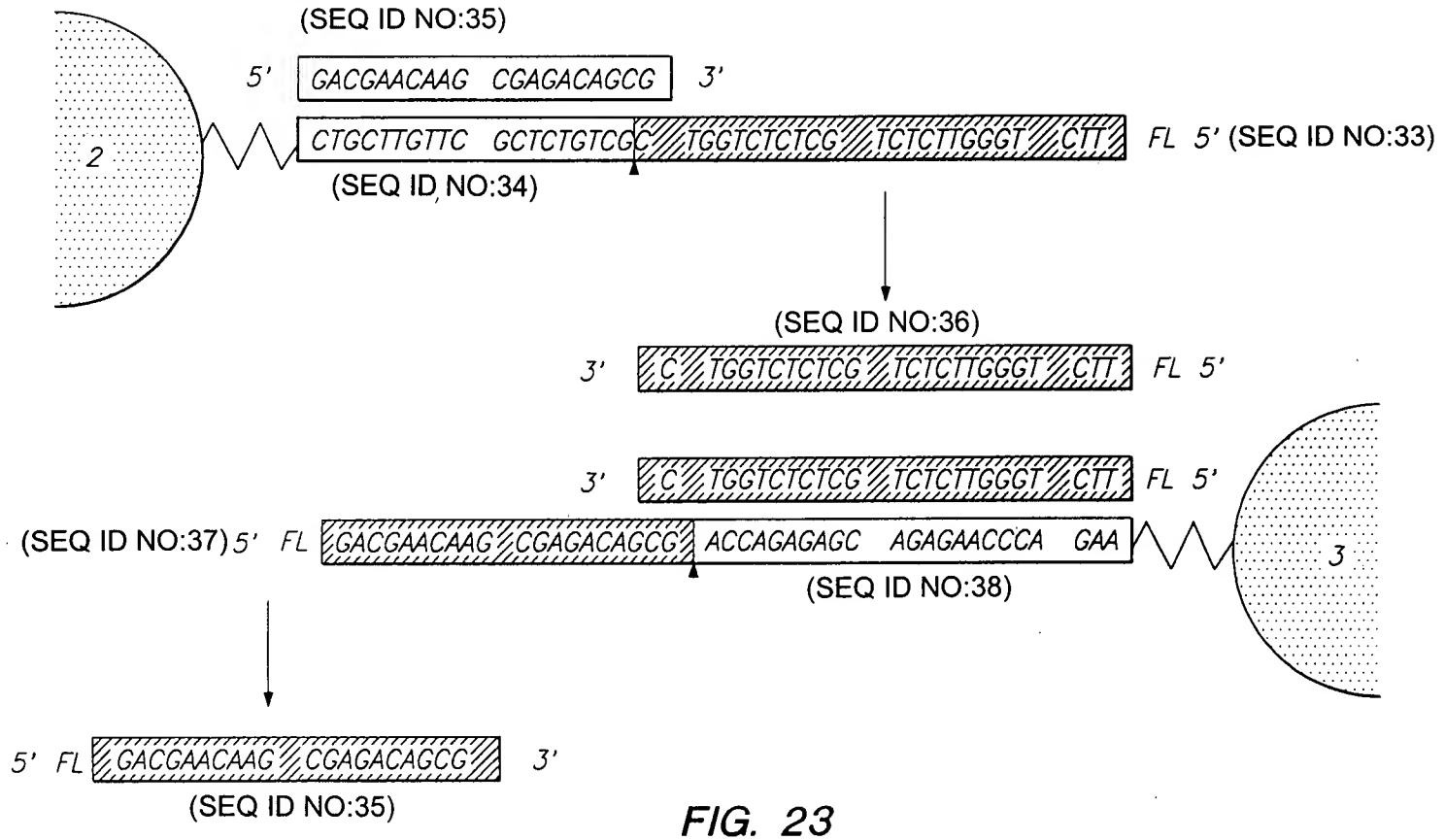

(SEQ ID NO:35)
5' GACGAACAAG CGAGACAGCG 3'
2
CTGCTTGTTC GCTCTGTCGC TGGTCTCTCG TCTCTTGGGT CTT FL 5' (SEQ ID NO:33)
(SEQ ID NO:34)
(SEQ ID NO:36)
3' C TGGTCTCTCG TCTCTTGGGT CTT FL 5'
3' C TGGTCTCTCG TCTCTTGGGT CTT FL 5'
(SEQ ID NO:37) 5' FL GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA
3
(SEQ ID NO:38)
5' FL GACGAACAAG CGAGACAGCG 3'
(SEQ ID NO:35)

FIG. 23

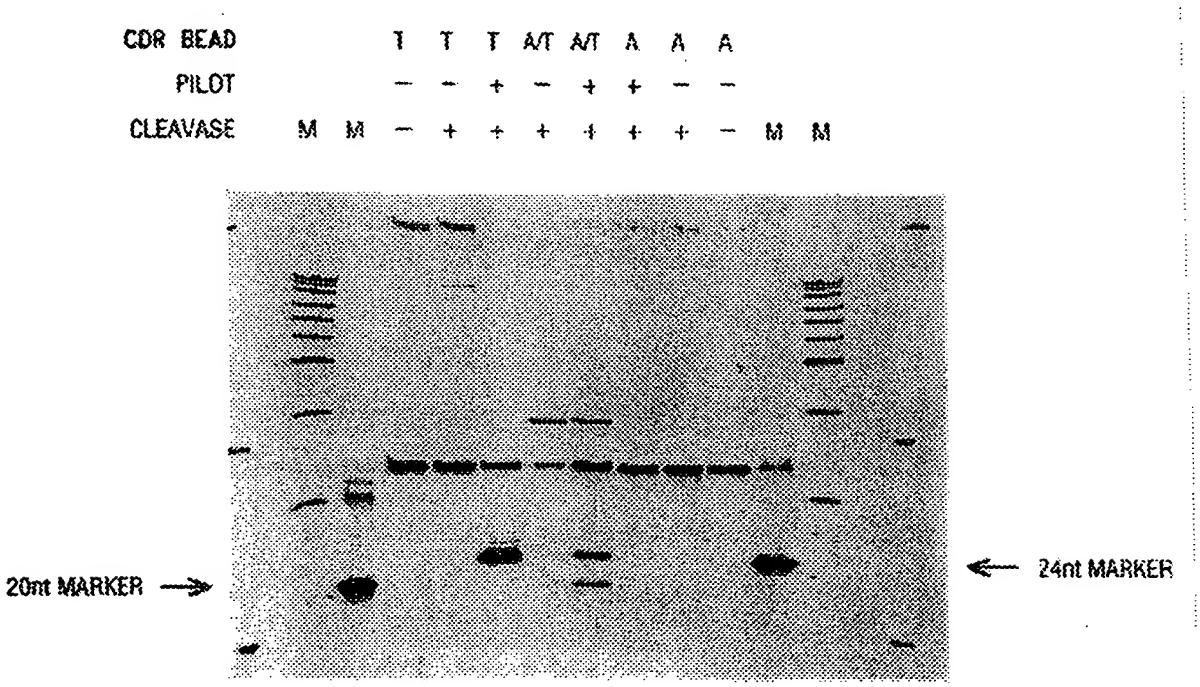

CDR BEAD T T T A/T A/T A A A
PILOT – – + – + + – –
CLEAVASE M M – + + + + + + – M M
20nt MARKER
24nt MARKER

FIG. 24

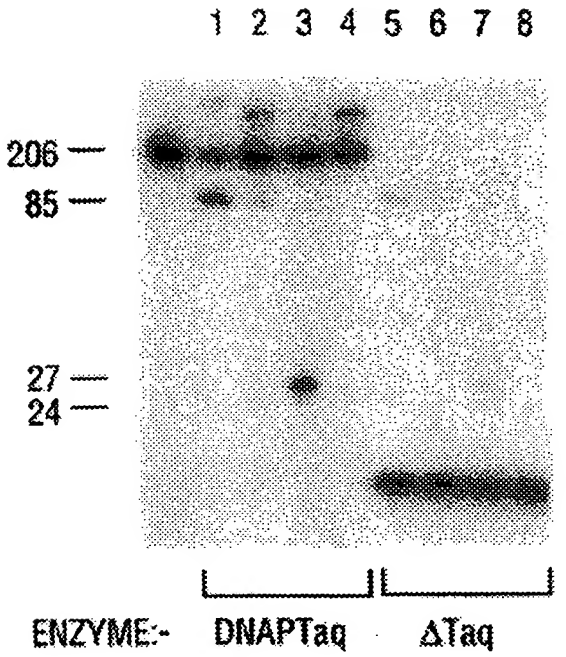


FIG. 25A

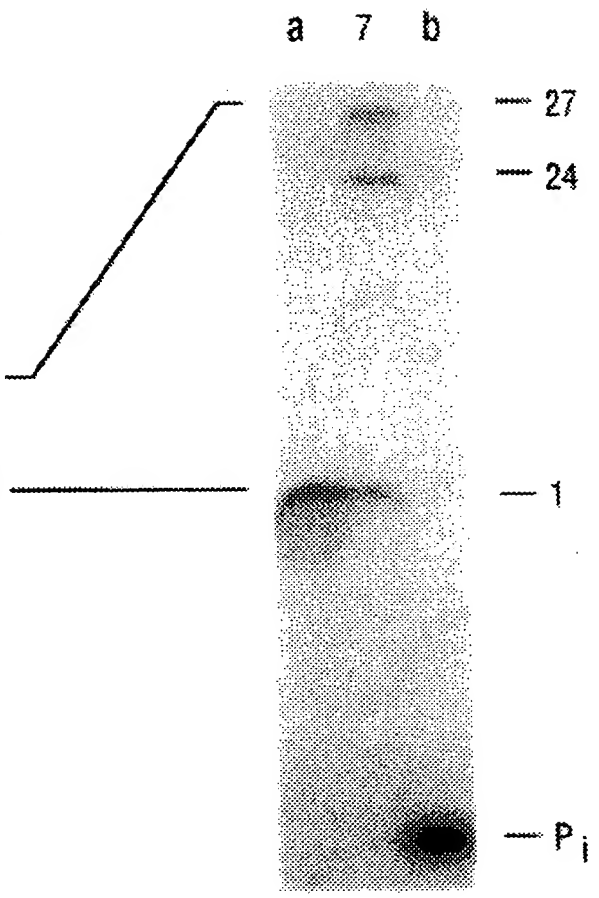


FIG. 25B

FIG. 26A

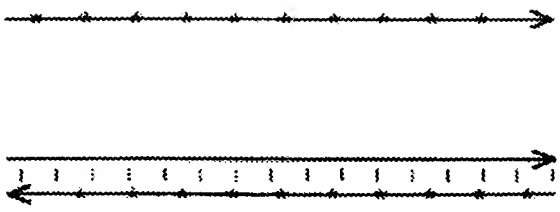
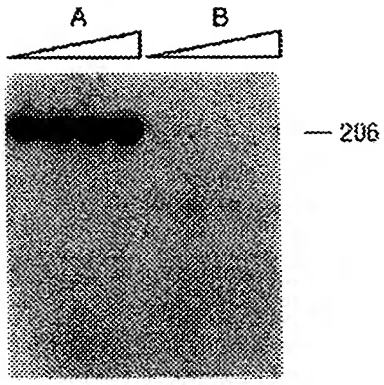


FIG. 26B

* = ^{32}P



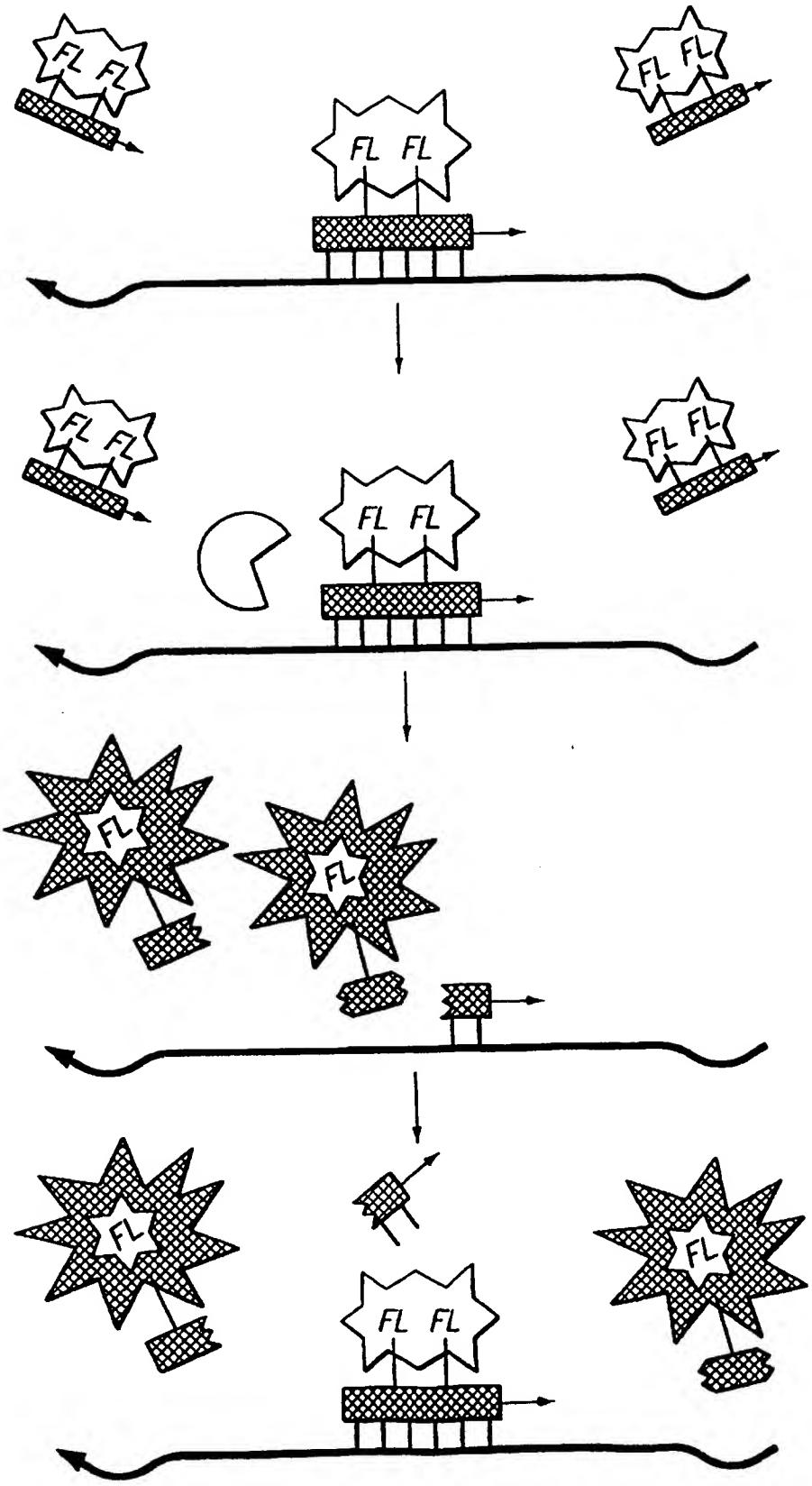


FIG. 27

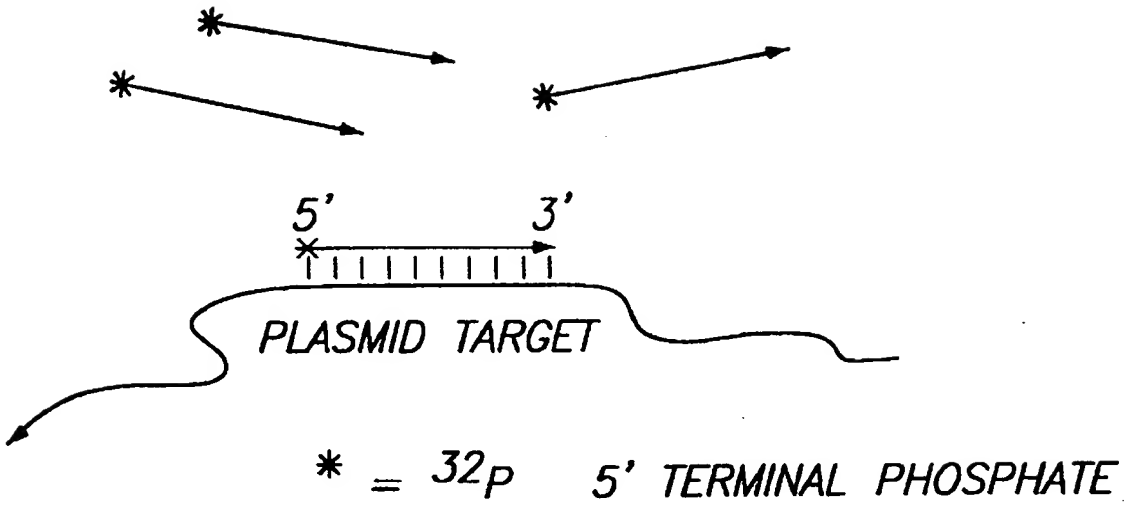


FIG. 28A

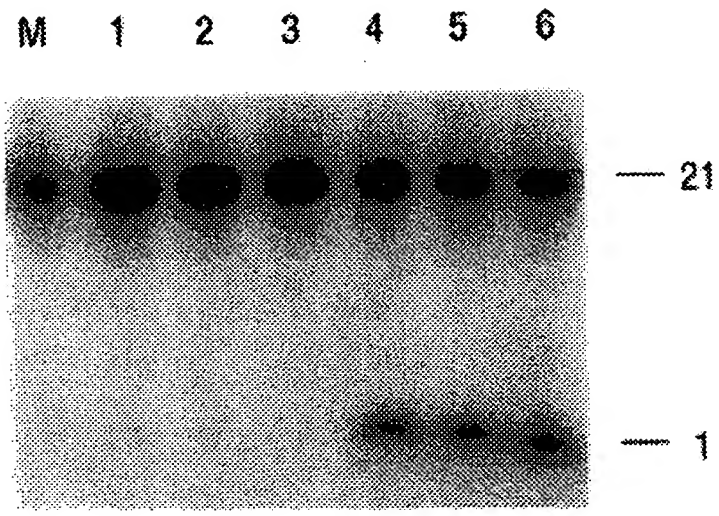


FIG. 28B

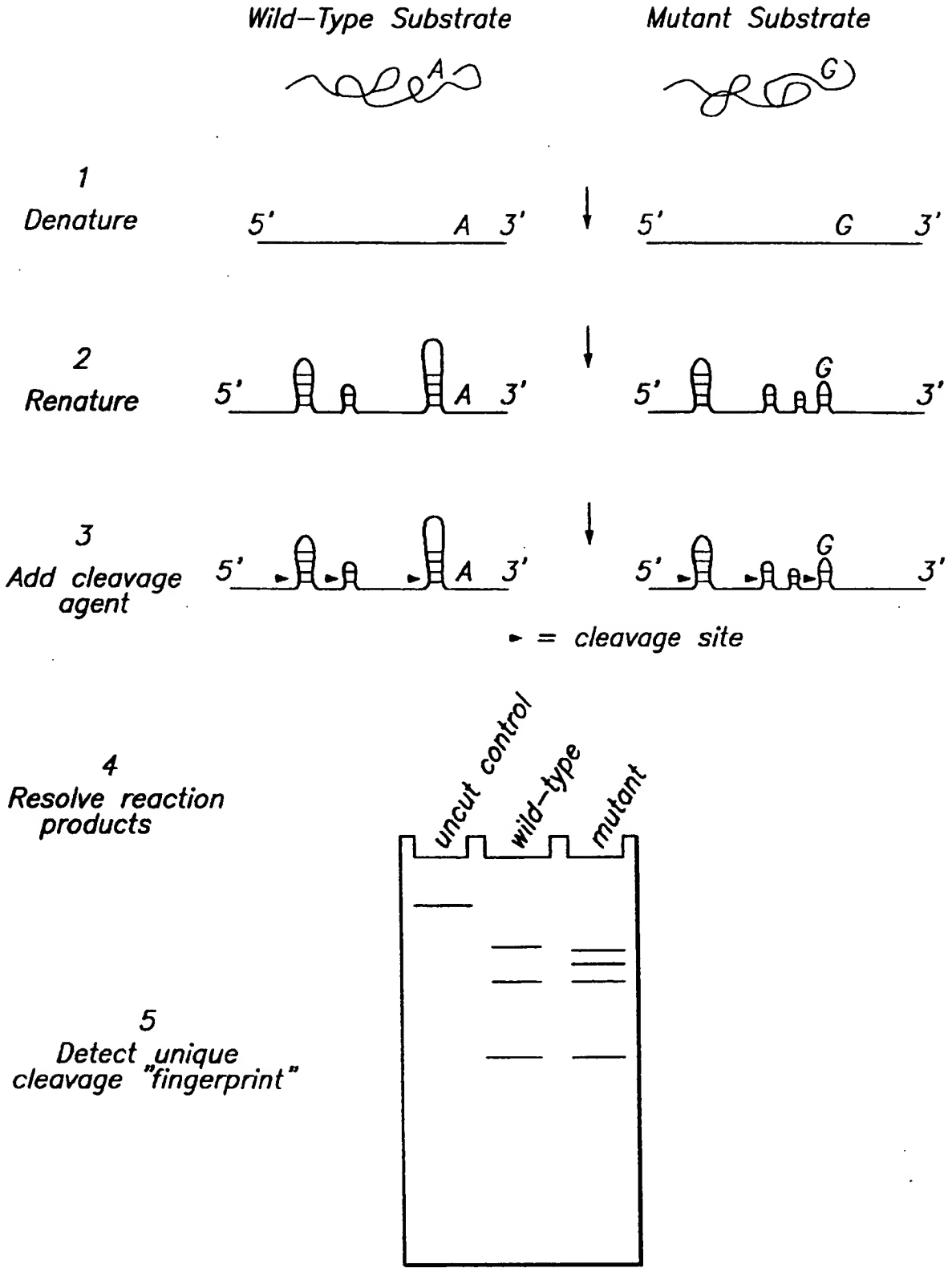

Wild–Type Substrate
Mutant Substrate
A
G
1
Denature
5'
A
3'
5'
G
3'
2
Renature
5'
A
3'
5'
G
3'
3
Add cleavage agent
5'
A
3'
5'
G
3'
► = cleavage site
4
Resolve reaction products
uncut control
wild–type
mutant
5
Detect unique cleavage "fingerprint"

FIG. 29

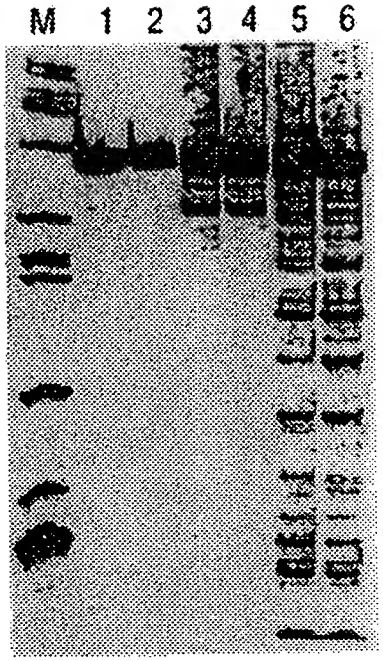


FIG. 30

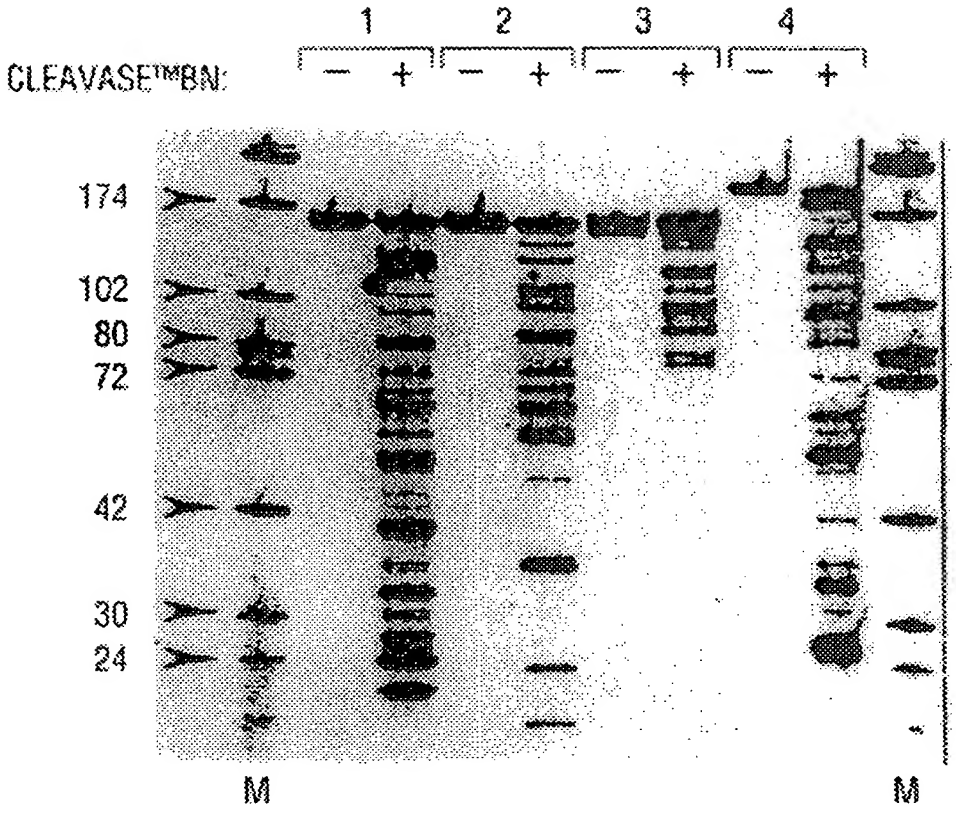


FIG. 31

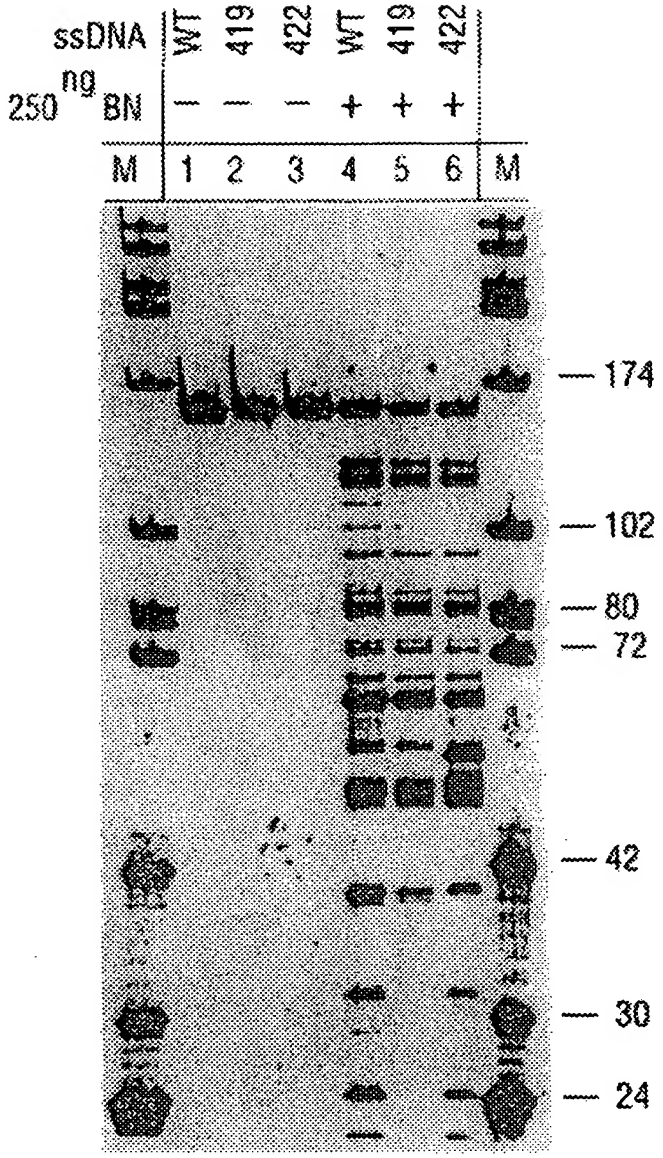

ssDNA
WT
419
422
WT
419
422
250 ng BN
– – – + + +
M 1 2 3 4 5 6 M
174
102
80
72
42
30
24

FIG. 32

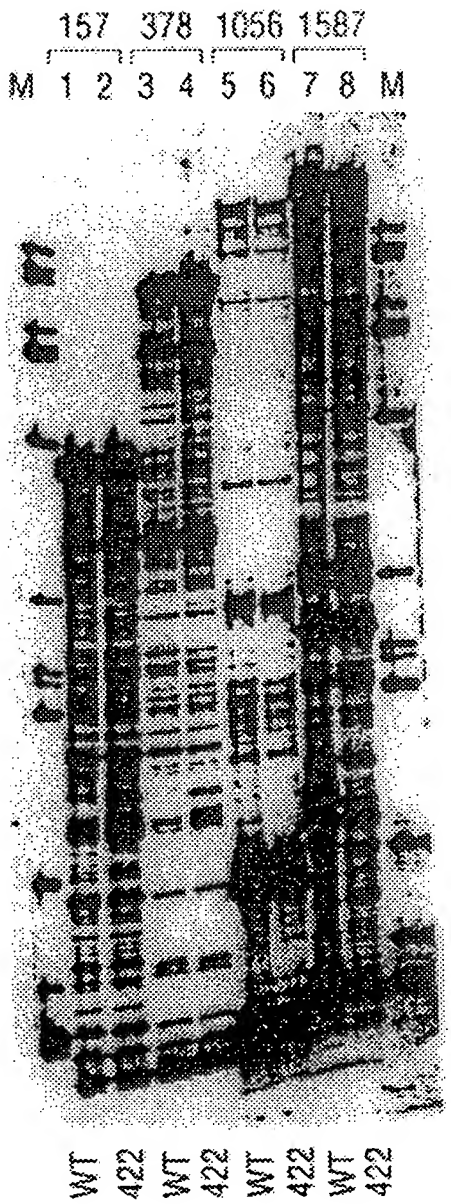


FIG. 33

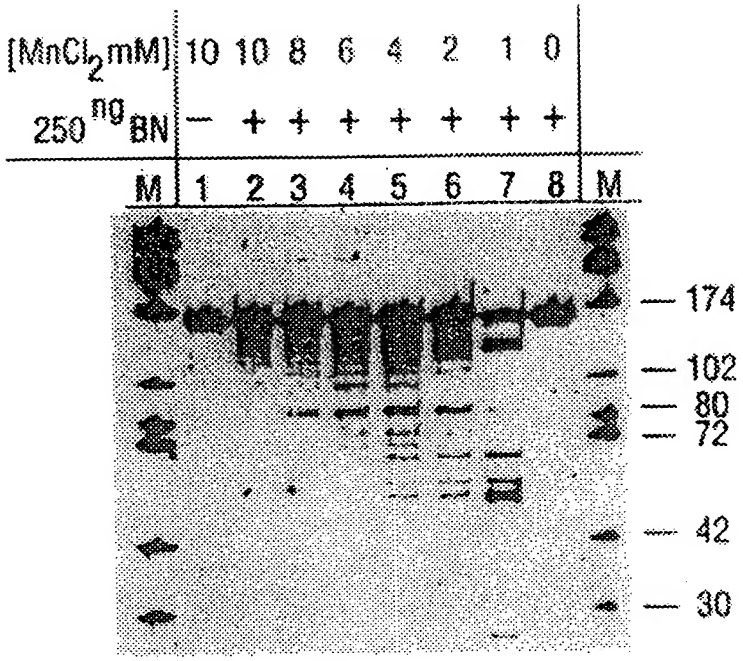


FIG. 34

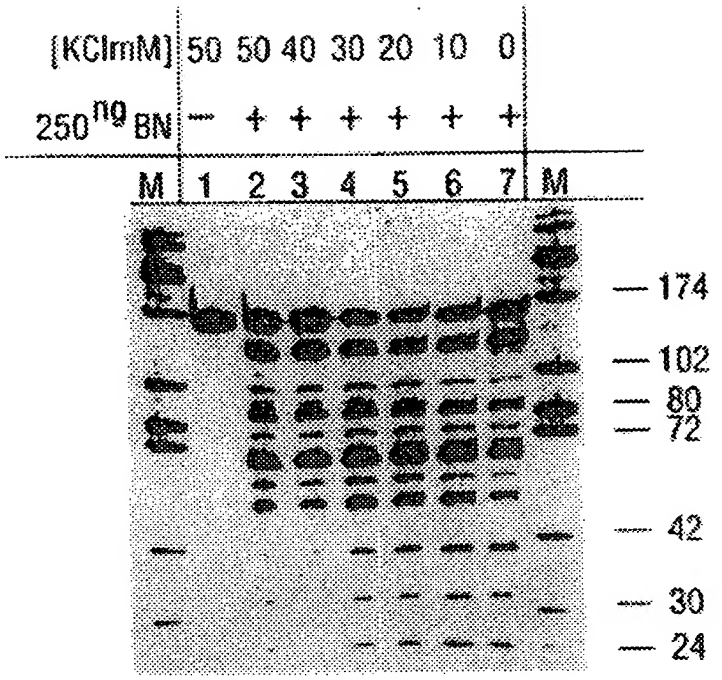


FIG. 35

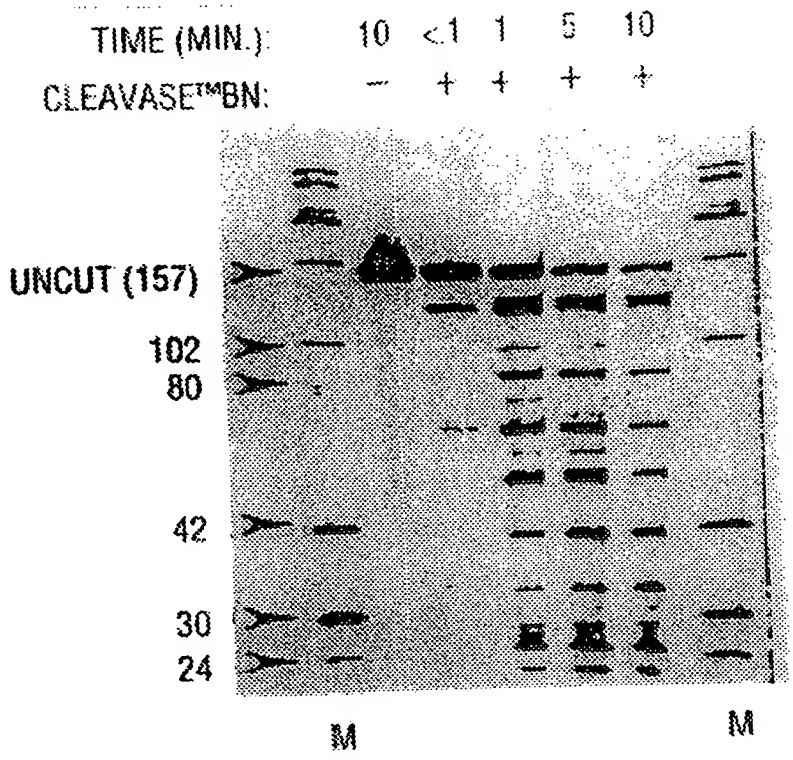


FIG. 36

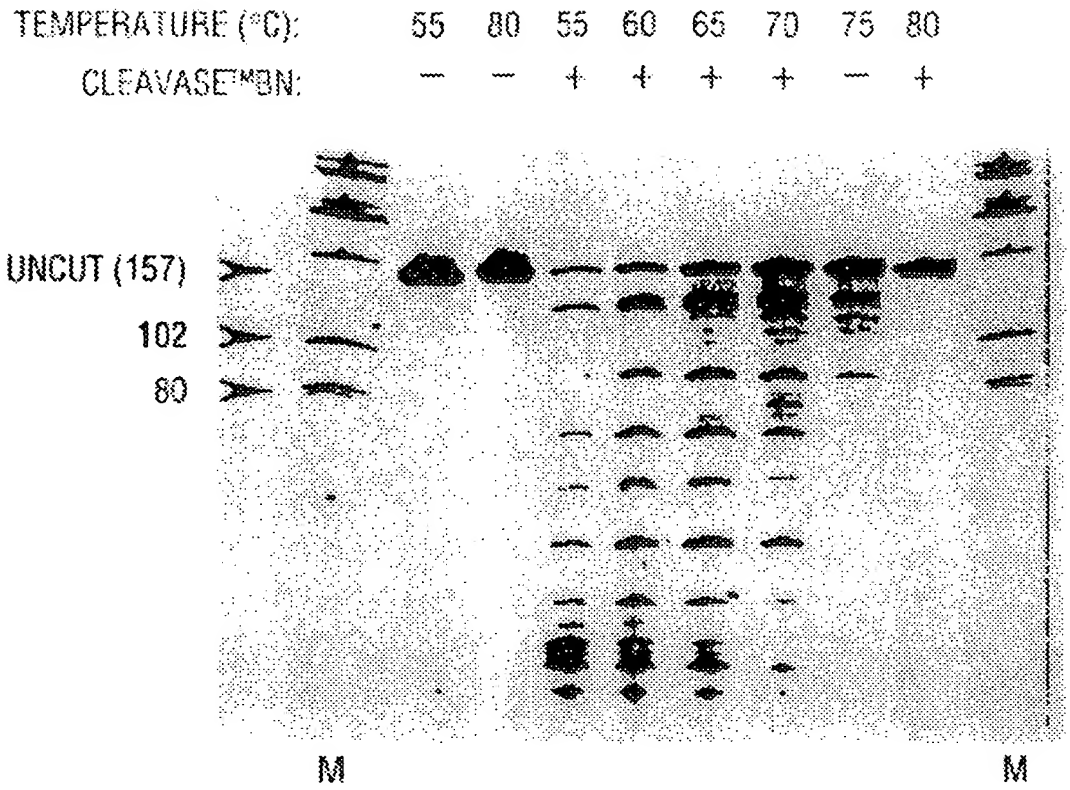

TEMPERATURE (°C): 55 80 55 60 65 70 75 80
CLEAVASE™BN: — — + + + + — +
UNCUT (157)
102
80
M
M

FIG. 37

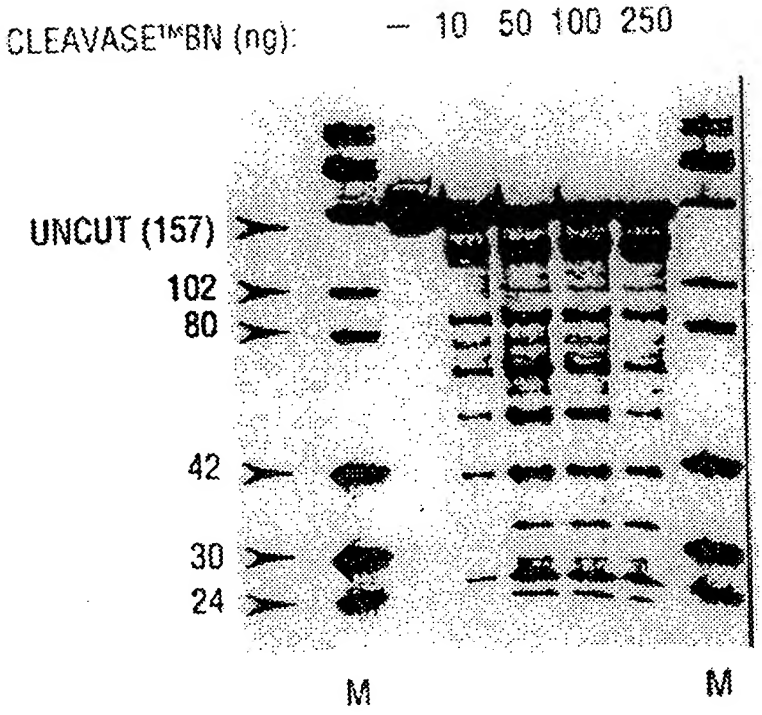


FIG. 38

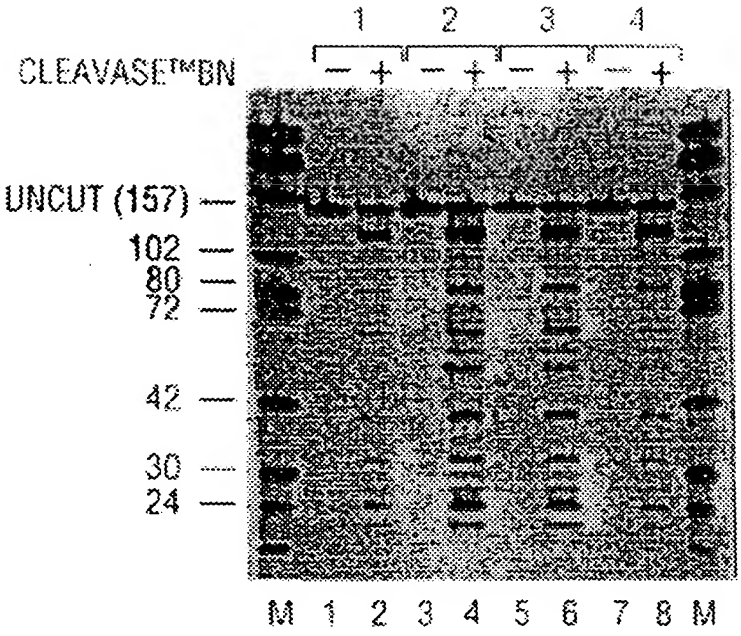


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCEIN ANTI-SENSE STRAND					
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ng BN	–	–	–	+	+	+	+	+	+	–	–	–
M	1	2	3	4	5	6	7	8	9	10	11	12

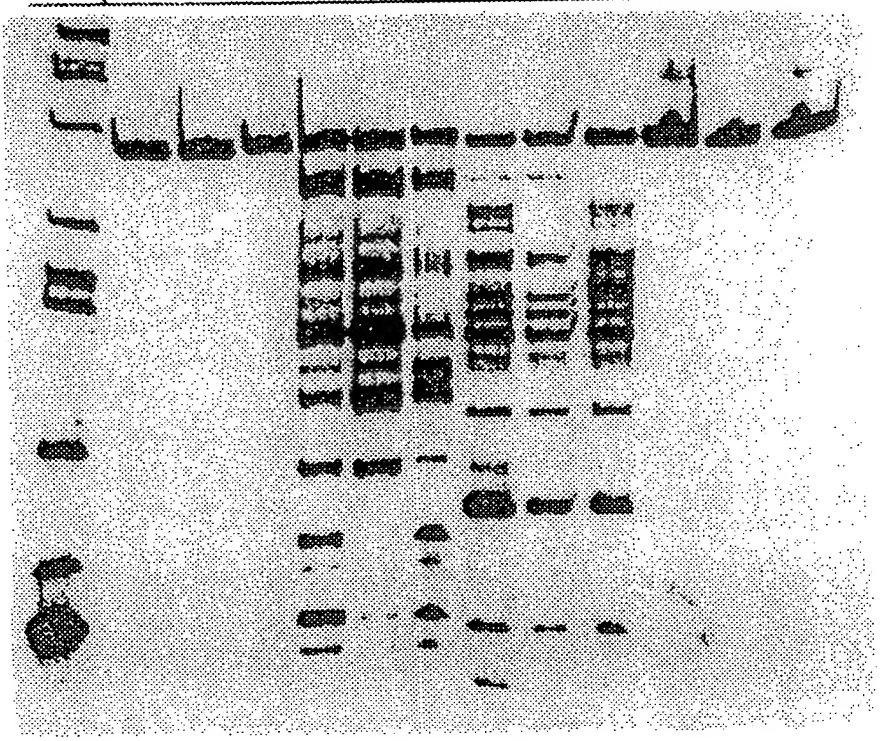


FIG. 40

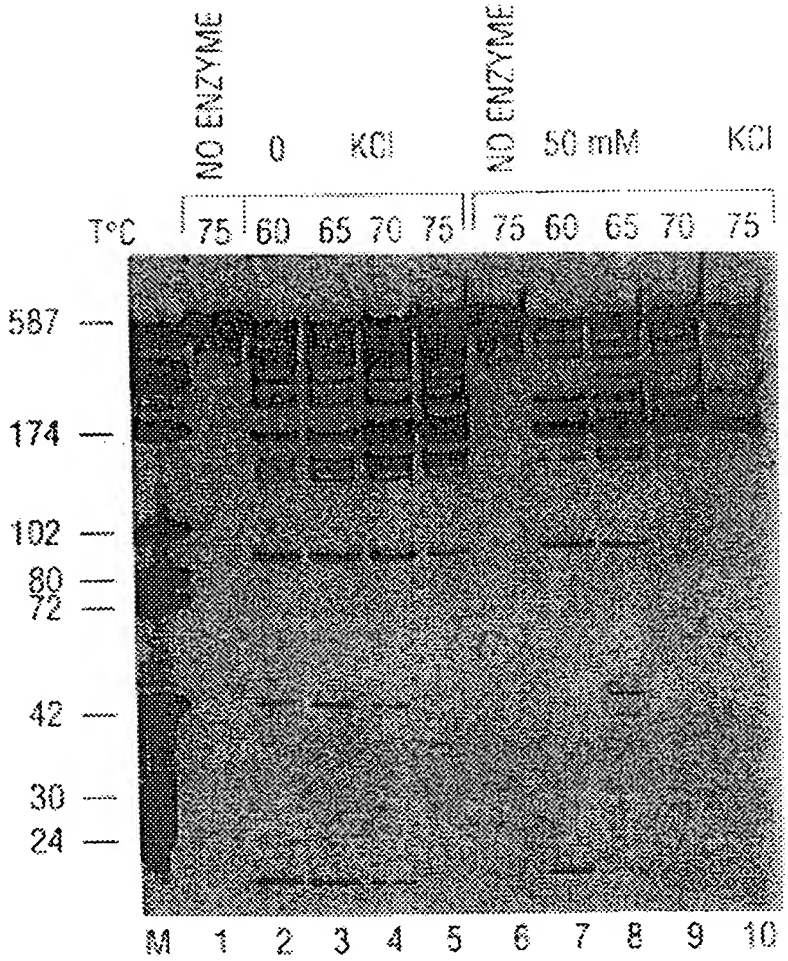

NO ENZYME
0 KCl
NO ENZYME
50 mM KCl
T°C
75 60 65 70 75 75 60 65 70 75
587
174
102
80
72
42
30
24
M 1 2 3 4 5 6 7 8 9 10

FIG. 41

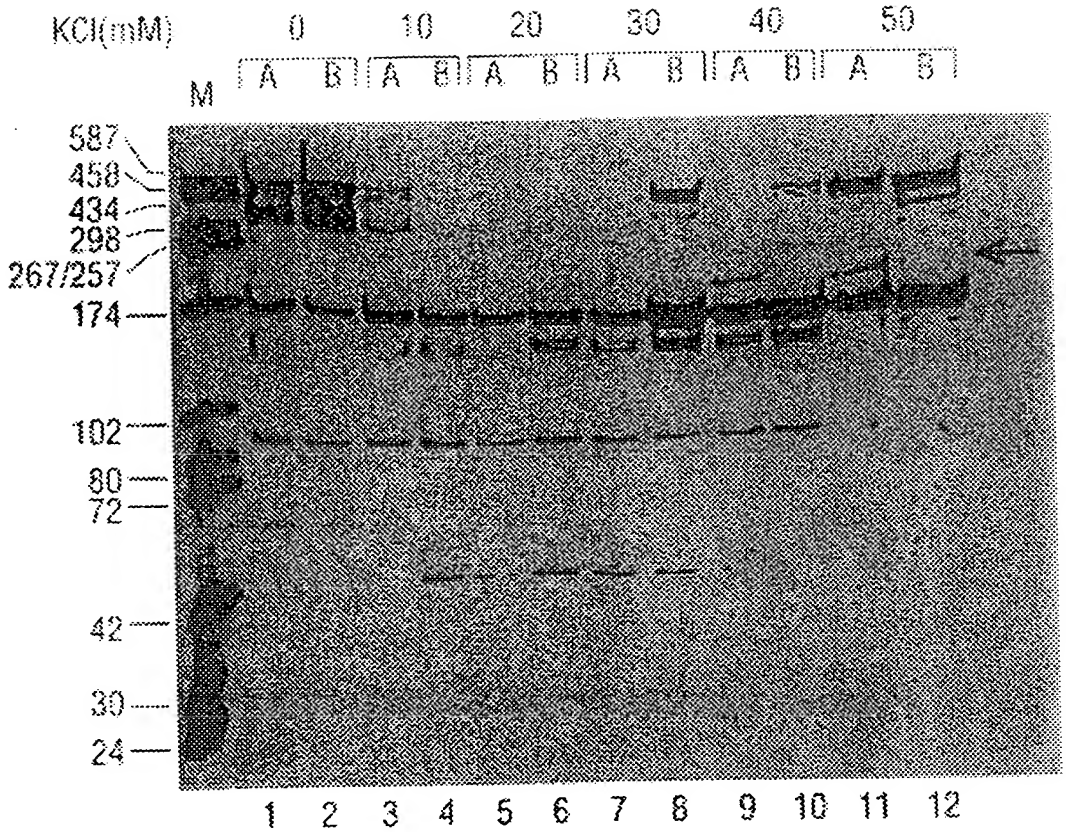

KCl(mM)
0
10
20
30
40
50
A
B
M
587
458
434
298
267/257
174
102
80
72
42
30
24
1
2
3
4
5
6
7
8
9
10
11
12

FIG. 42

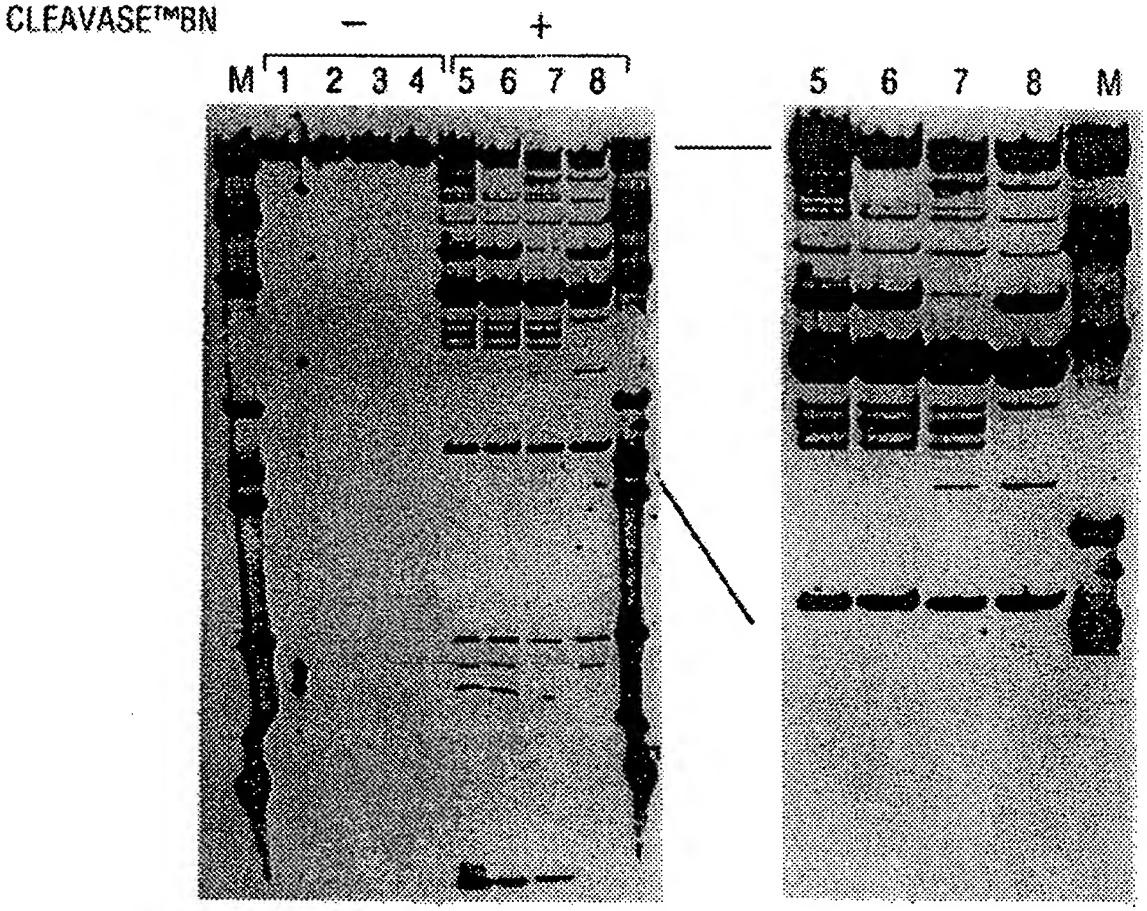


FIG. 43

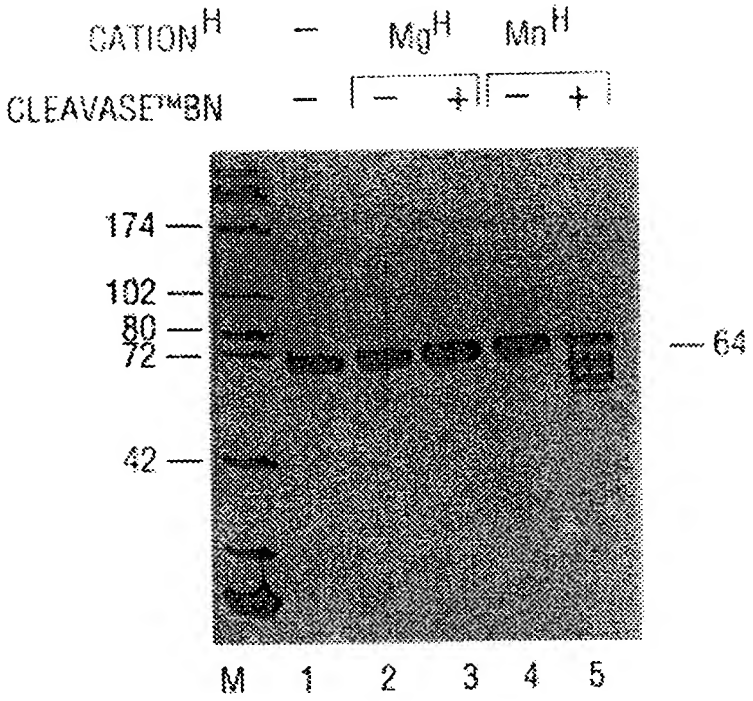


FIG. 44

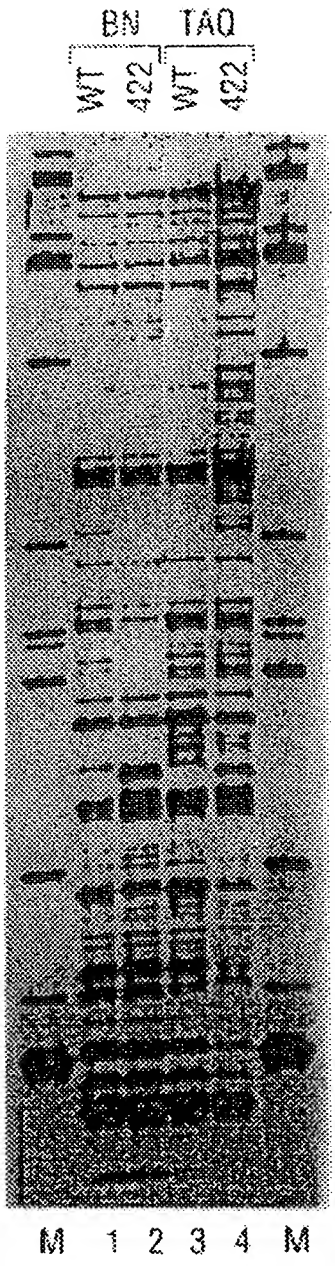


FIG. 45

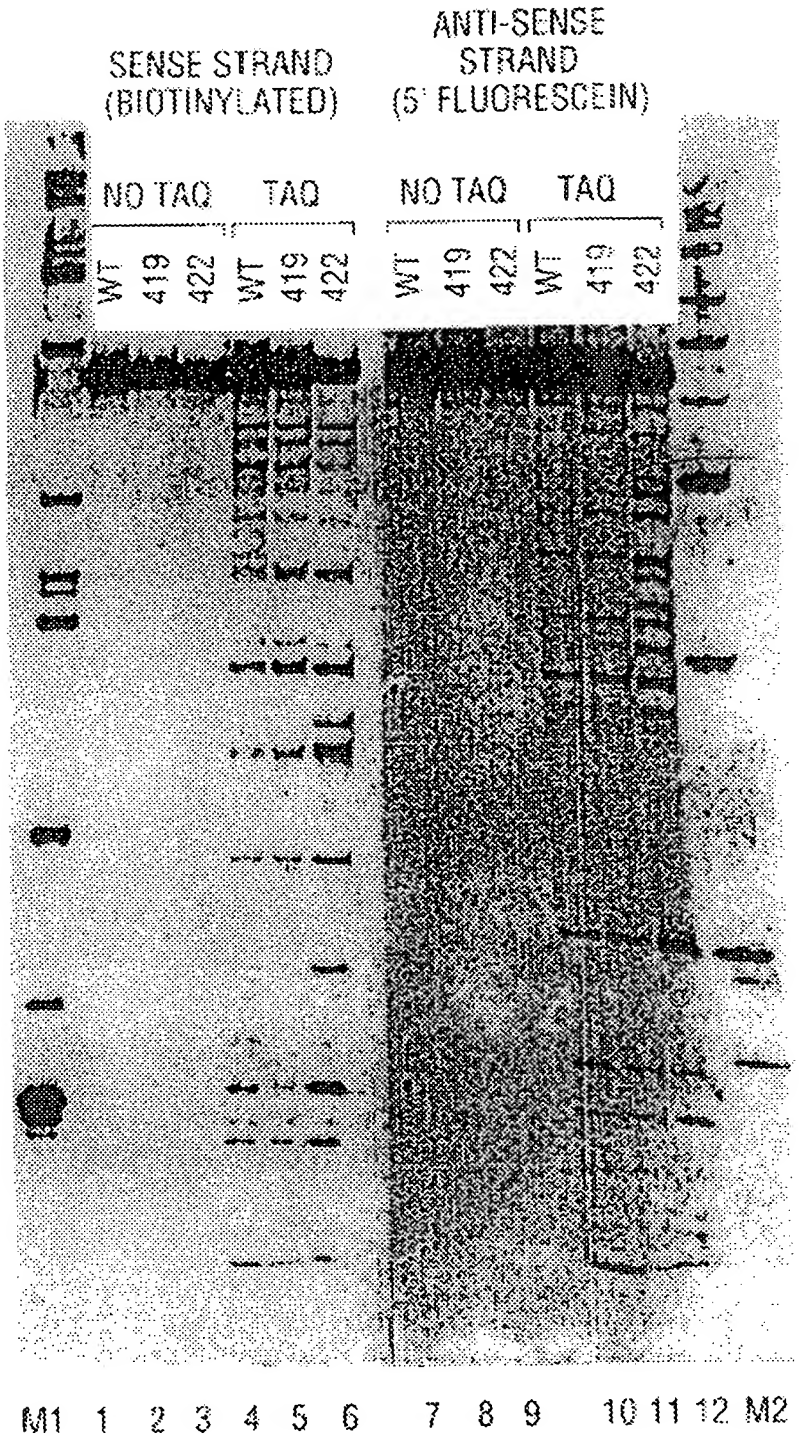

SENSE STRAND
(BIOTINYLATED)
ANTI-SENSE
STRAND
(5' FLUORESCEIN)
NO TAQ
TAQ
NO TAQ
TAQ
WT
419
422
WT
419
422
WT
419
422
WT
419
422
M1 1 2 3 4 5 6 7 8 9 10 11 12 M2

FIG. 46

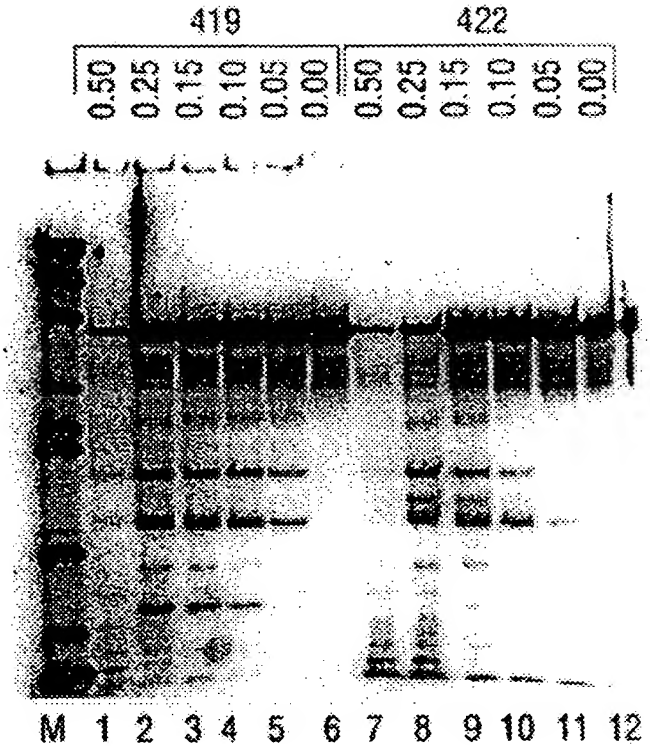

419
422
0.50
0.25
0.15
0.10
0.05
0.00
0.50
0.25
0.15
0.10
0.05
0.00
M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 47

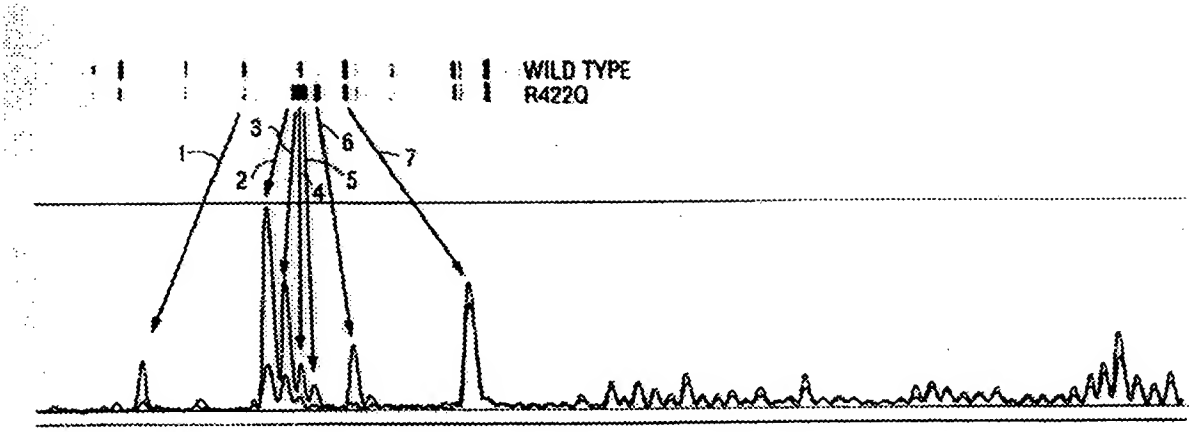


FIG. 48

L.100.8-1	5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 76)	3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC
L.46.16-10	5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 77)	3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC
L.46.16-12	5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 78)	3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC
L19.16-3	5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 79)	3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC
L.CEM/251	5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 80)	3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC
L.36.8-3	5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 81)	3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

```
                                                                  100
L.100.8-1          ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 76)    TACAATGCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA

L.46.16-10         ATGTTATGGGGAGG----------AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 77)    TACAATACCCCTCC----------TCGGCCAGCCCTTGTGGGTGAAAGA

L.46.16-12         ATGTTATGGGGAGG----------AGCCGGTCGGGAACACCCACTTTCT
(SEQ ID NO: 78)    TACAATACCCCTCC----------TCGGCCAGCCCTTGTGGGTGAAAGA

L19.16-3           ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCCCTCTCT
(SEQ ID NO: 19)    TACAATGCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGGAGAGA

L.CEM/251          ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT
(SEQ ID NO: 80)    TACAATGCCCCTCCATGACCCTTCCTCGGCCAGCCCTTGCGGGTGAAAGA

L.36.8-3           ATGTTACGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT
(SEQ ID NO: 81)    TACAATGCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA
```

FIG. 49B

150

L.100.8-1	5'TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L.46.16-10	5'TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L.46.16-12	5'TGGTGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L.19.16-3	5'TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L.CEM/251	5'TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT
L.36.8-3	5'TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGCGGA
	3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

FIG. 49C

		200
L.100.8-1	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG	
	CTCCGACCGTCTAACTCGGGACCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-10	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGCTAG	
	CTCCGACCGTCTAACTCGGGACCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.46.16-12	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG	
	CTCCGACCGTCTAACTCGGGACCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.19.16-3	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG	
	CTCCGACCGTCTAACTCGGGACCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.CEM/251	GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG	
	CTCCGACCGTCTAACTCGGGACCCTCCAAGAGAGGTCGTGATCGTCCATC	
L.36.8-3	GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG	
	CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC	

FIG. 49D

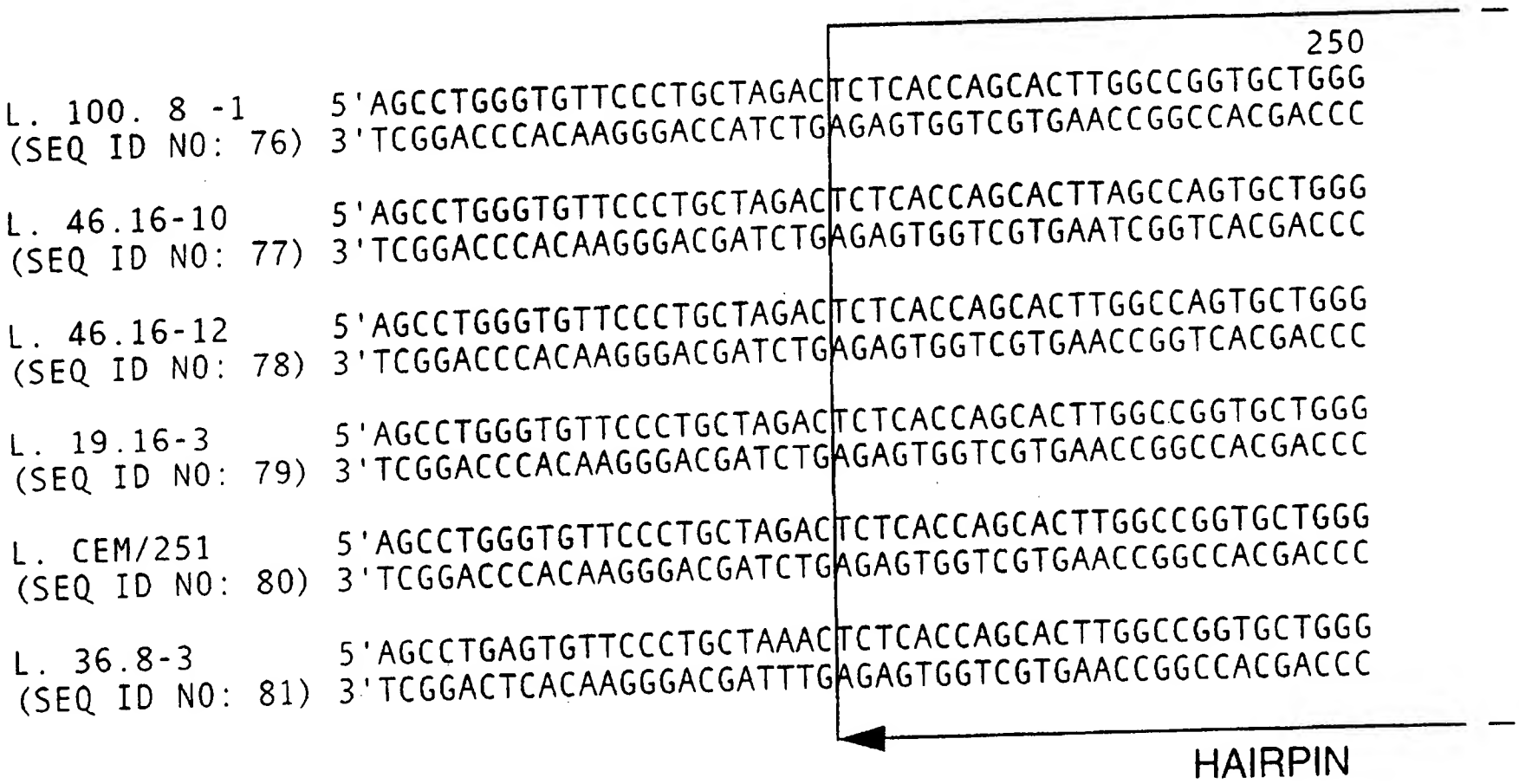

250
L. 100. 8 -1
(SEQ ID NO: 76)
5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG
3'TCGGACCCACAAGGGACCATCTGAGAGTGGTCGTGAACCGGCCACGACCC
L. 46.16-10
(SEQ ID NO: 77)
5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTAGCCAGTGCTGGG
3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAATCGGTCACGACCC
L. 46.16-12
(SEQ ID NO: 78)
5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCAGTGCTGGG
3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGTCACGACCC
L. 19.16-3
(SEQ ID NO: 79)
5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG
3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC
L. CEM/251
(SEQ ID NO: 80)
5'AGCCTGGGTGTTCCCTGCTAGACTCTCACCAGCACTTGGCCGGTGCTGGG
3'TCGGACCCACAAGGGACGATCTGAGAGTGGTCGTGAACCGGCCACGACCC
L. 36.8-3
(SEQ ID NO: 81)
5'AGCCTGAGTGTTCCCTGCTAAACTCTCACCAGCACTTGGCCGGTGCTGGG
3'TCGGACTCACAAGGGACGATTTGAGAGTGGTCGTGAACCGGCCACGACCC
HAIRPIN

FIG. 49E

```
                                                              300
L. 100. 8 -1          CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(SEQ ID NO: 76)       GTCTCACCGAGGTGCGAACGAACGAATTTCTGGAGAAGTTATTTCGACGC

L. 46.16-10           CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(SEQ ID NO: 77)       GTCTCACCGAGGTGCGAACGAACGAATTTCTGGAGAAGTTATTTCGACGG

L. 46.16-12           CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(SEQ ID NO: 78)       GTCTCACCGAGGTGCGAACGAACGAATTTCTGGAGAAGTTATTTCGACGG

L. 19.16-3            CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(SEQ ID NO: 79)       GTCTCACCGAGGTGCGAACGAACGAATTTCTGGAGAAGTTATTTCGACGG

L. CEM/251            CAGAGTGACTCCACGCTTGCTTGCTTAAAGCCCTCTTCAATAAAGCTGCC
(SEQ ID NO: 80)       GTCTCACTGAGGTGCGAACGAACGAATTTCGGGAGAAGTTATTTCGACGG

L. 36.8-3             CAGAGCGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(SEQ ID NO: 81)       GTCTCGCCGAGGTGCGAACGAACGAATTTCTGGAGAAGTTATTTCGACGG
```

HAIRPIN

FIG. 49F

```
                                                                  350
L.100.8-1       5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATCCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'

L.46,16-10      5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'

L.46.16-12      5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'

L.19,16-3       5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'

L.CEM/251       5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATTCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'

L.36.8-3        5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCCTG  G 3'
                3'TAAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCGGCGGAC  C 5'
```

FIG. 49G

FIG. 50

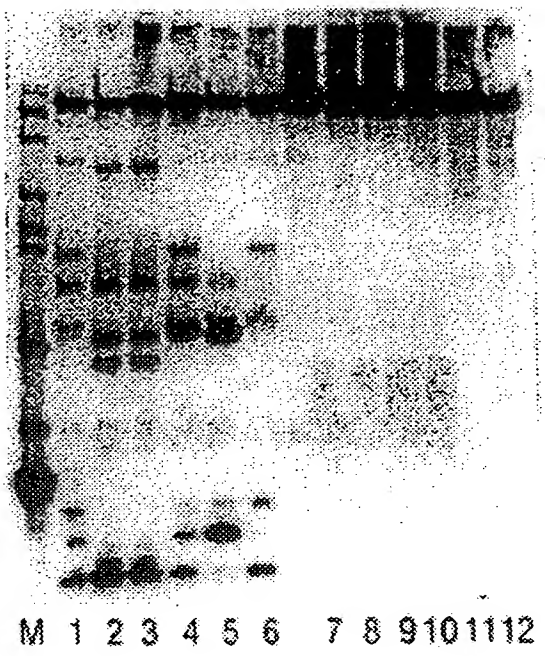


FIG. 51

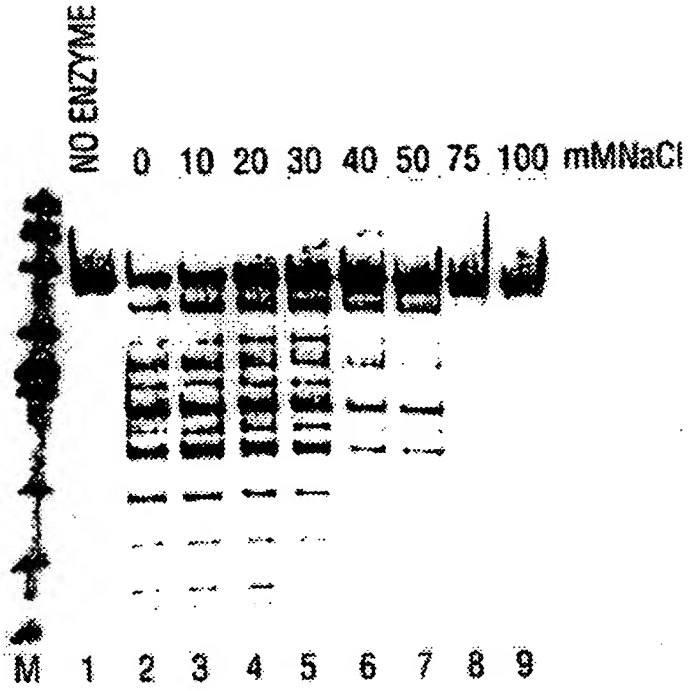


FIG. 52

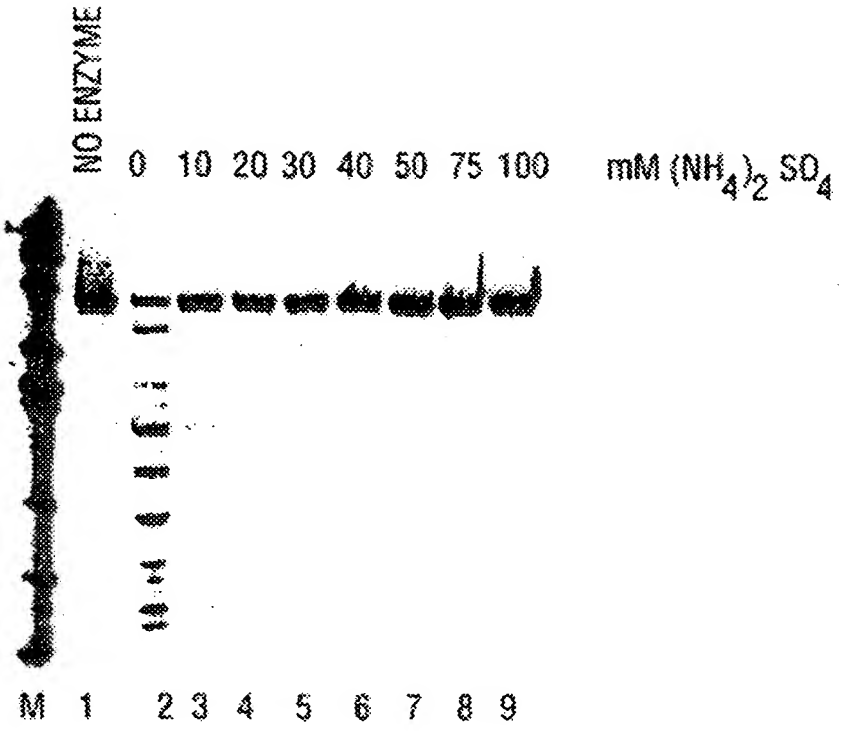


FIG. 53

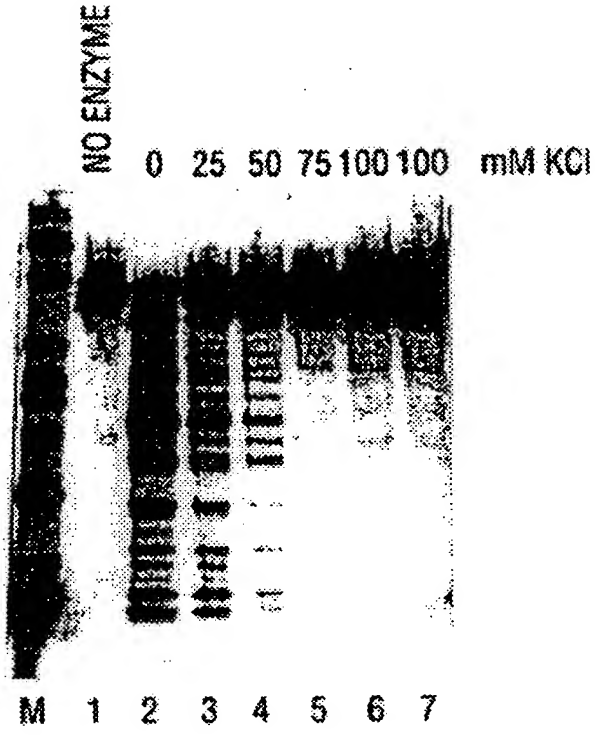


FIG. 54

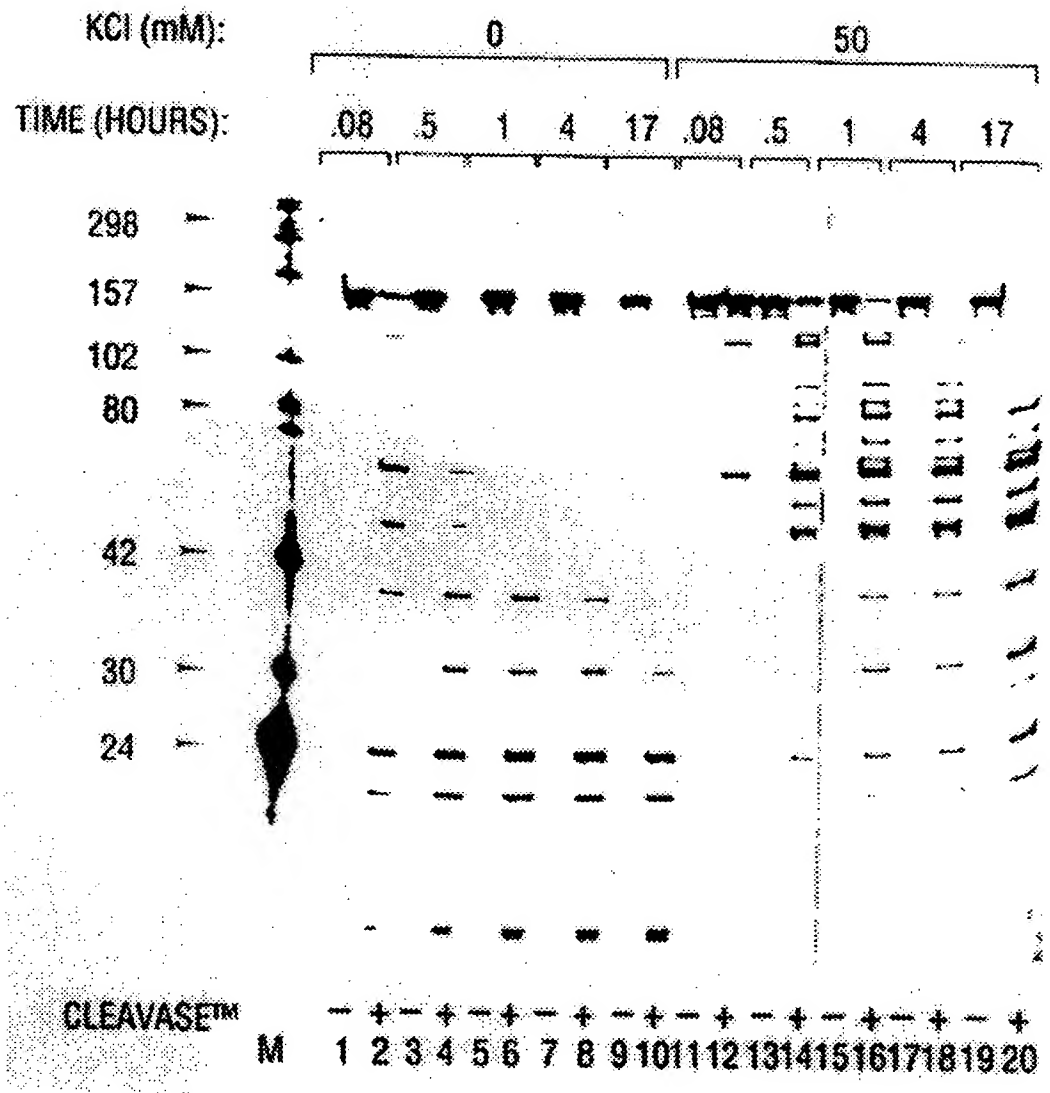

KCl (mM):
0
50
TIME (HOURS):
.08 .5 1 4 17 .08 .5 1 4 17
298
157
102
80
42
30
24
CLEAVASE™
M
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

FIG. 55

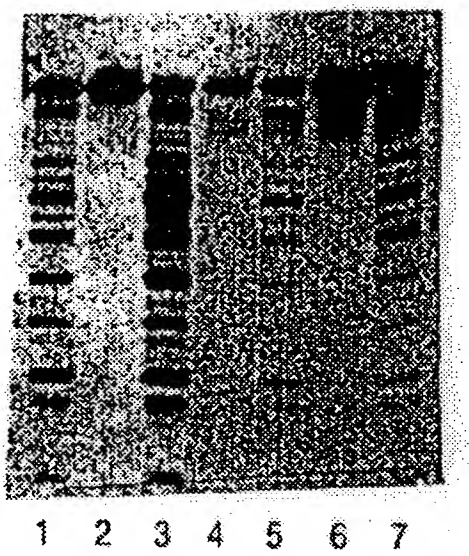


FIG. 56

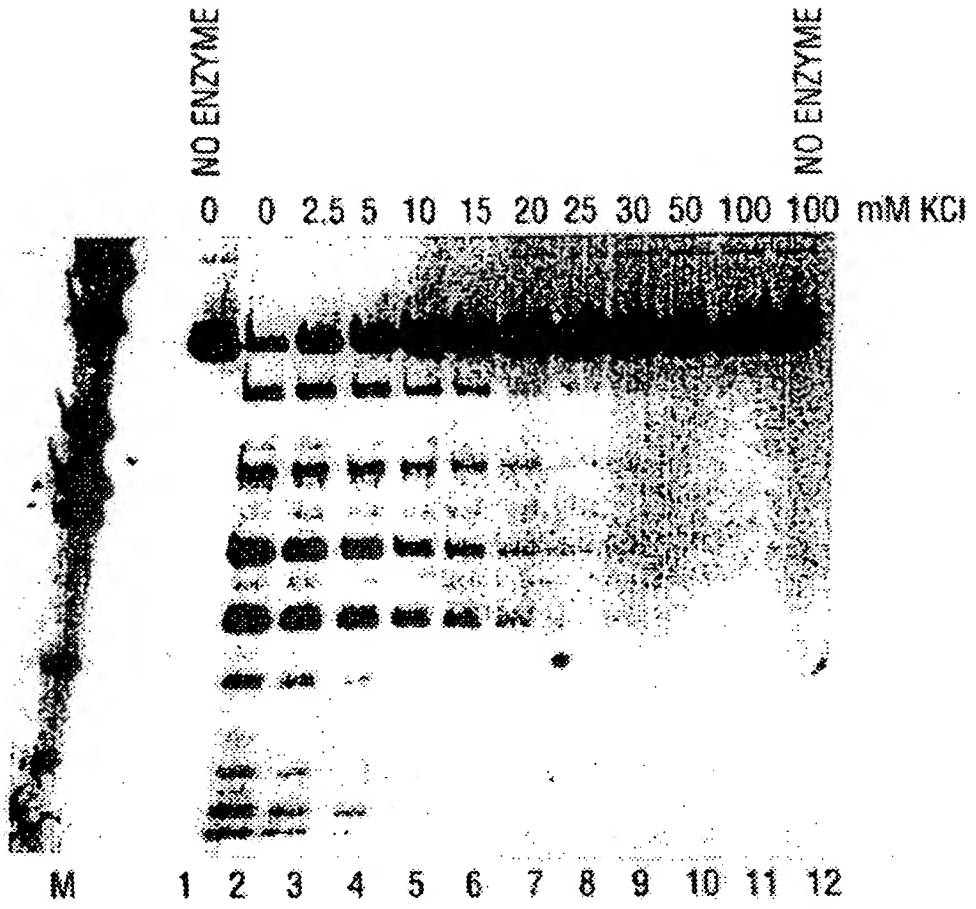

NO ENZYME
NO ENZYME
0 0 2.5 5 10 15 20 25 30 50 100 100 mM KCl
M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 57

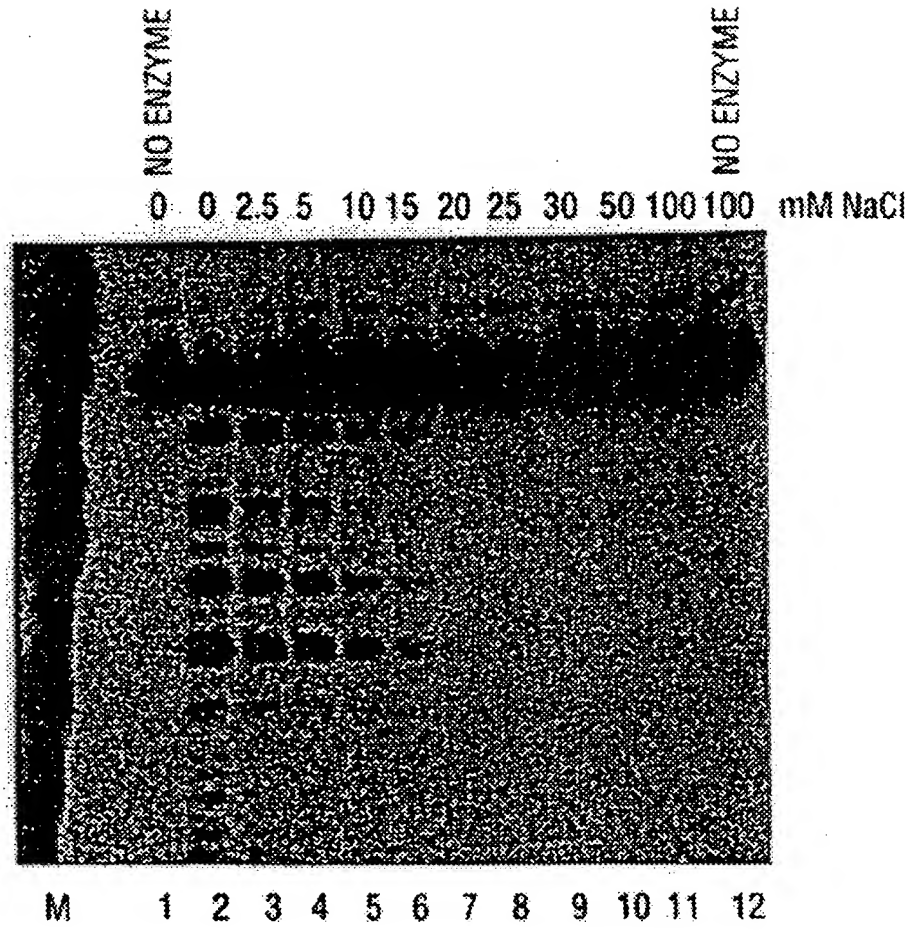

NO ENZYME
NO ENZYME
0 0 2.5 5 10 15 20 25 30 50 100 100 mM NaCl
M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 58

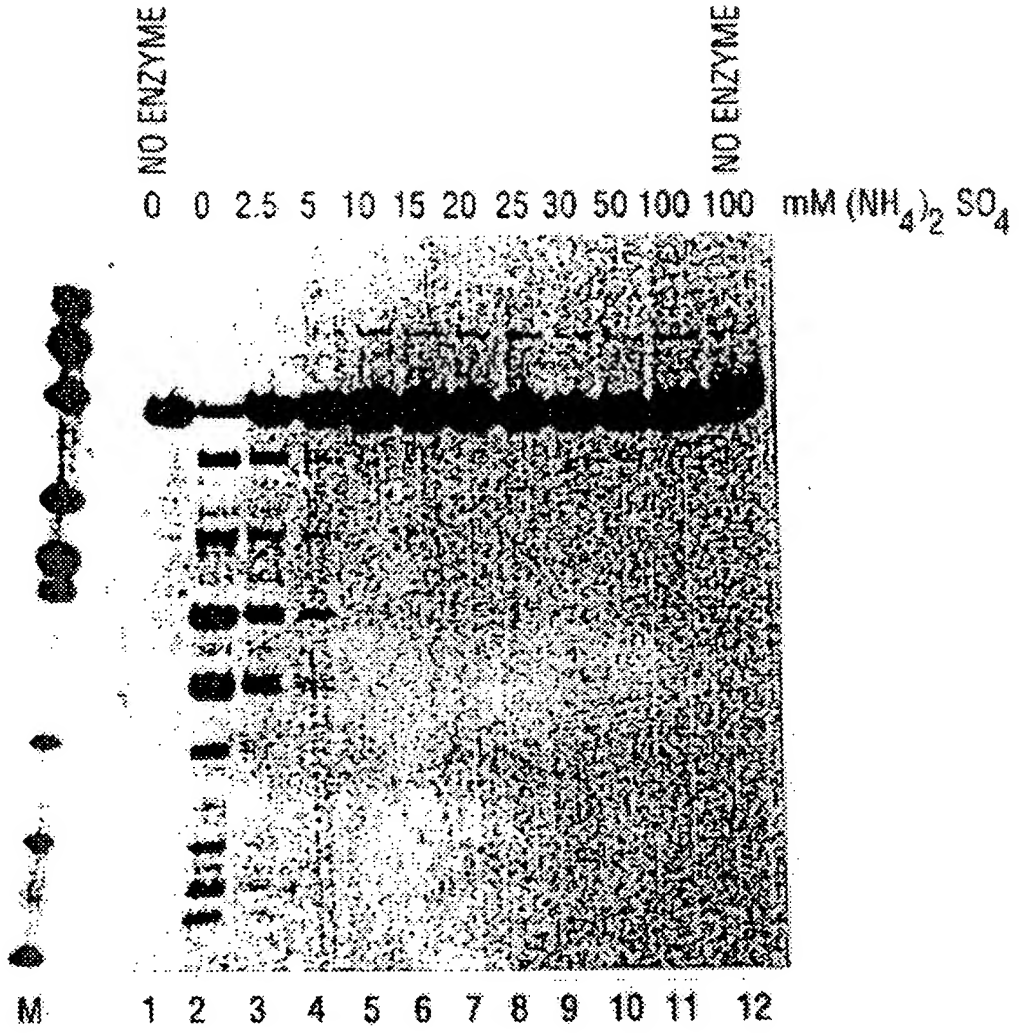

NO ENZYME
NO ENZYME
0 0 2.5 5 10 15 20 25 30 50 100 100 mM $(NH_4)_2$ SO_4
M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 59

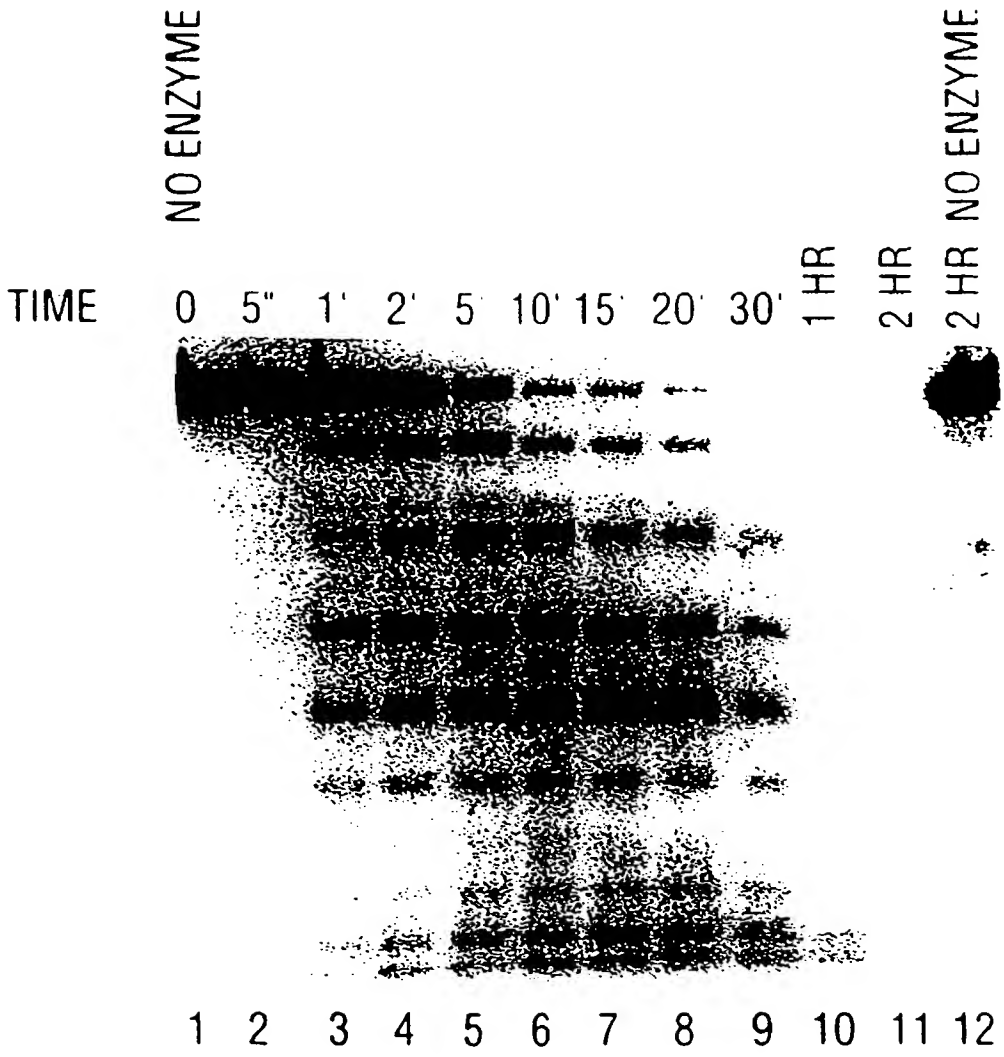


FIG. 60

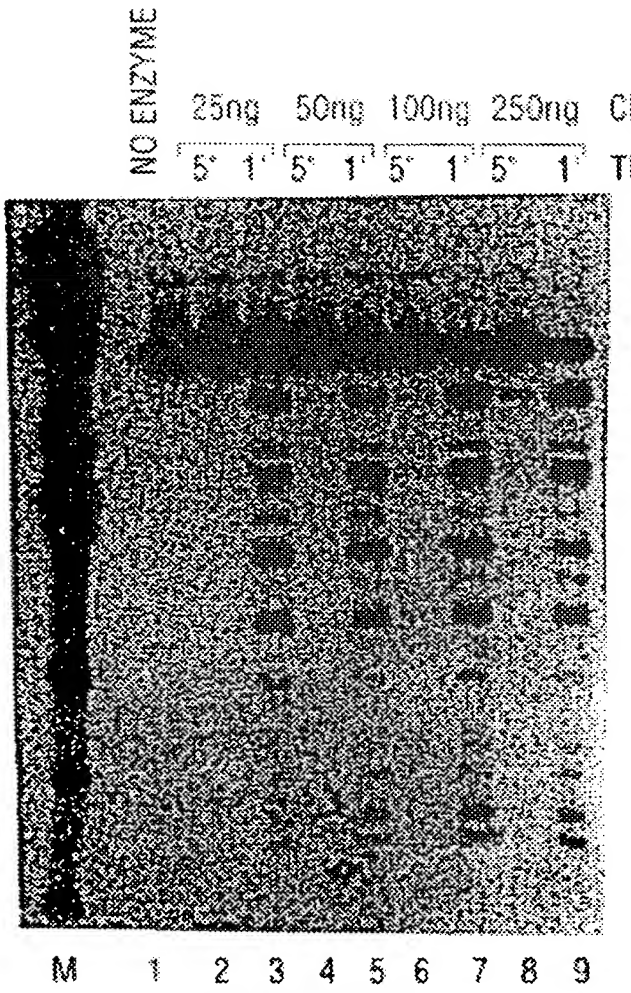

NO ENZYME
25ng
50ng
100ng
250ng
CLEAVASE™BN
5' 1' 5' 1' 5' 1' 5' 1'
TIME
M 1 2 3 4 5 6 7 8 9

FIG. 61

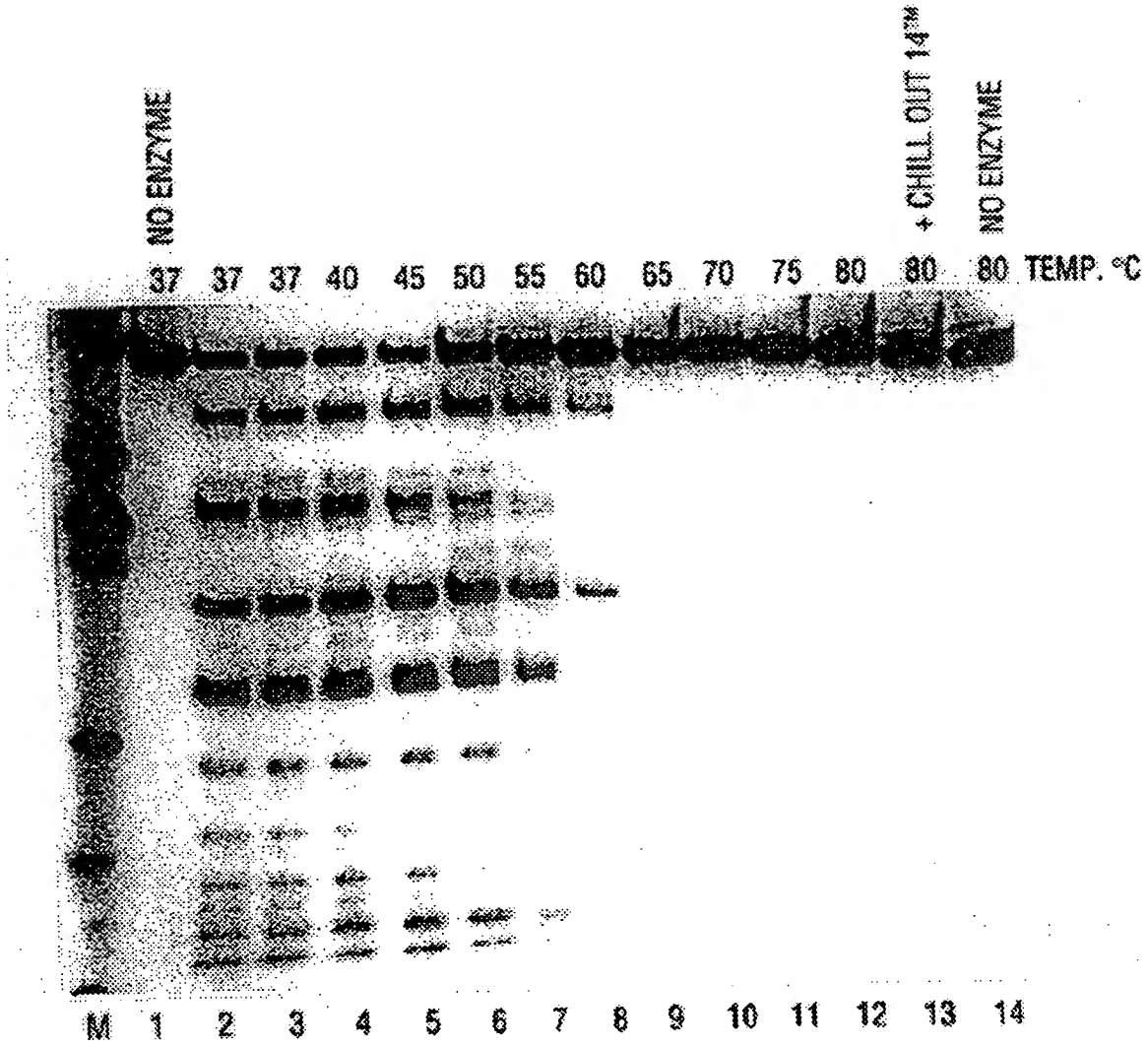


FIG. 62

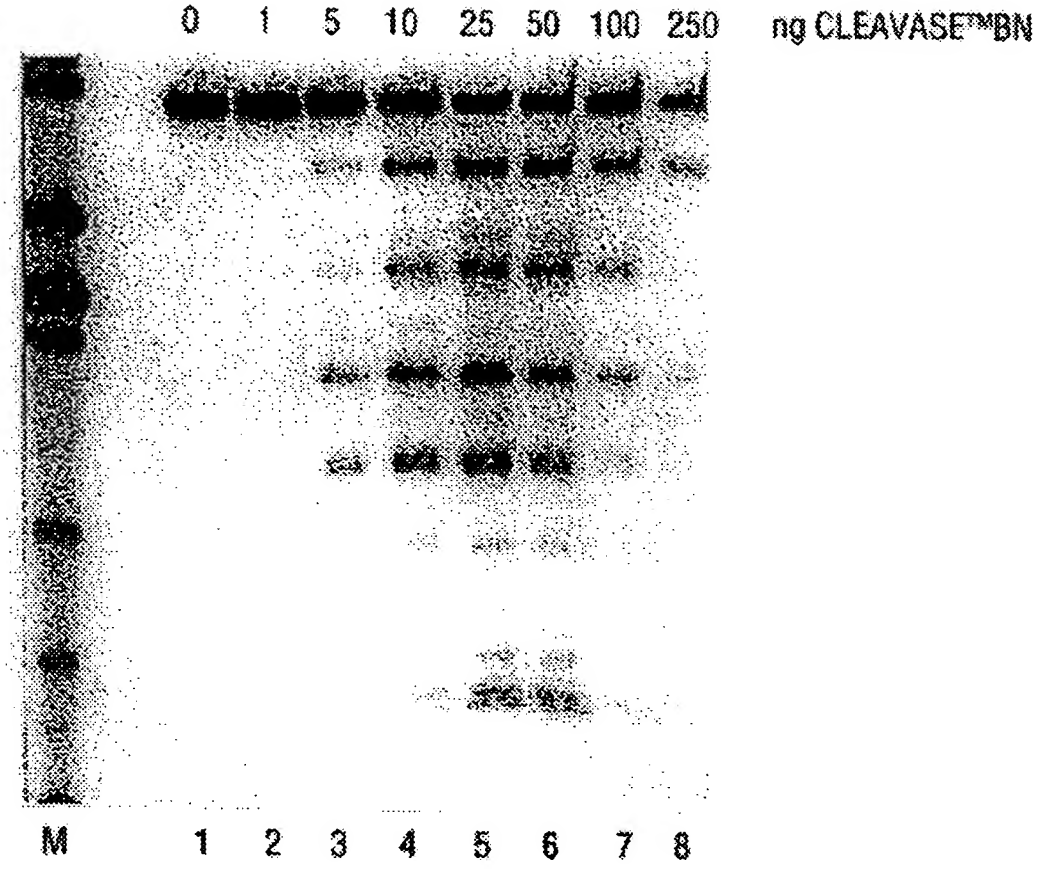


FIG. 63

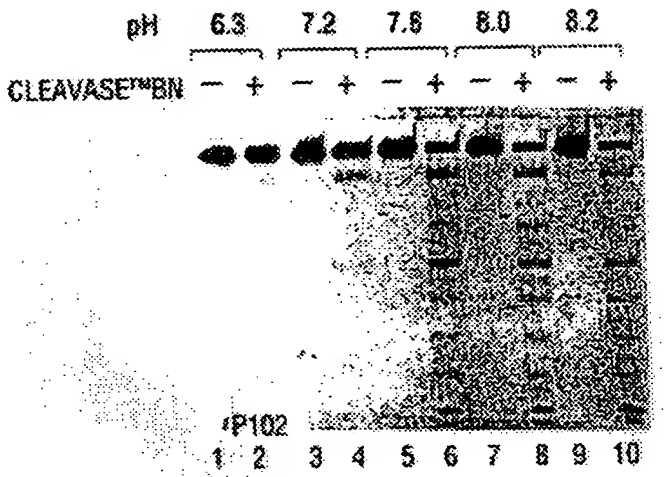


FIG. 64A

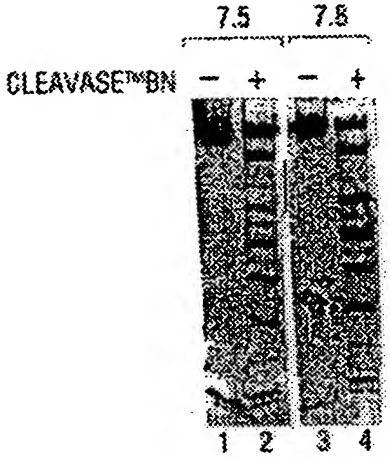


FIG. 64B

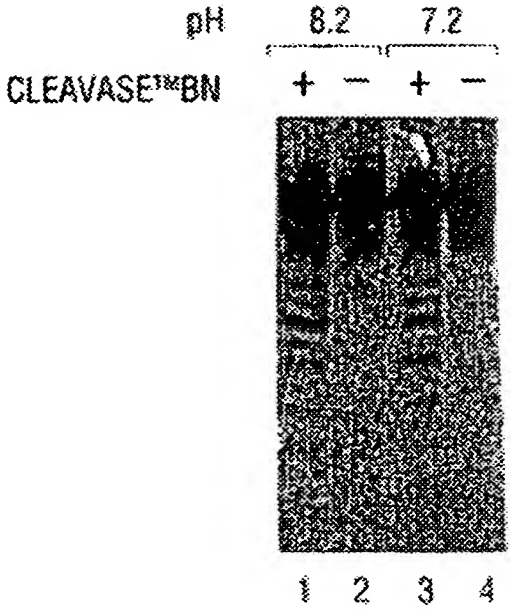


FIG. 65A

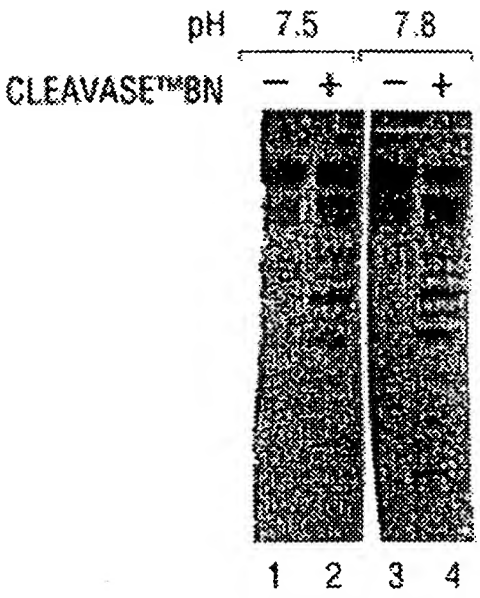


FIG. 65B

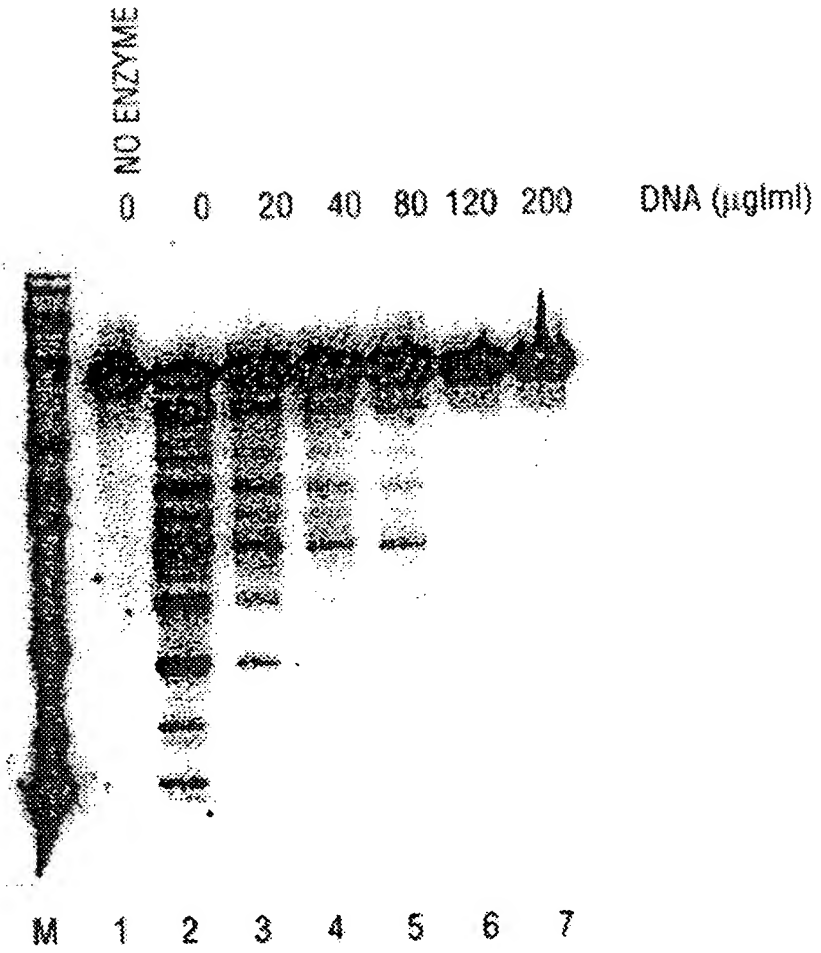


FIG. 66

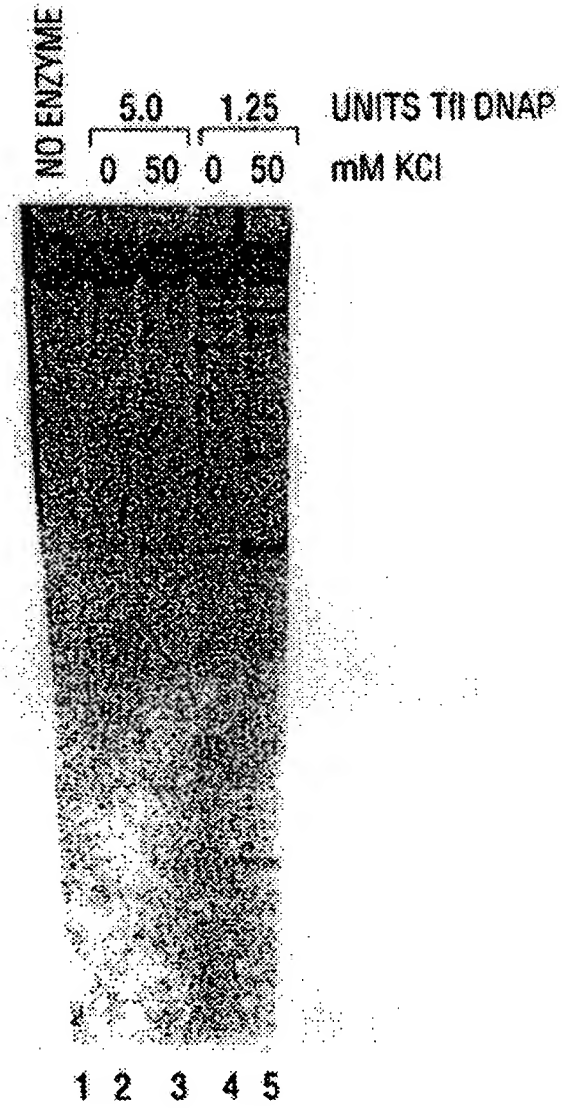


FIG. 67

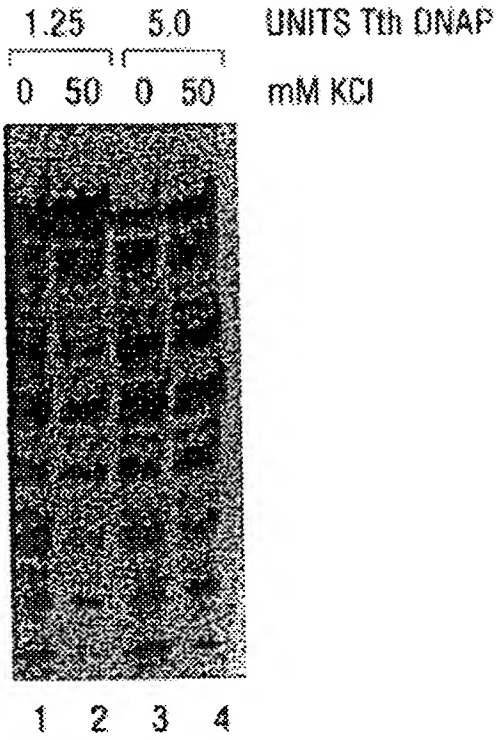


FIG. 68

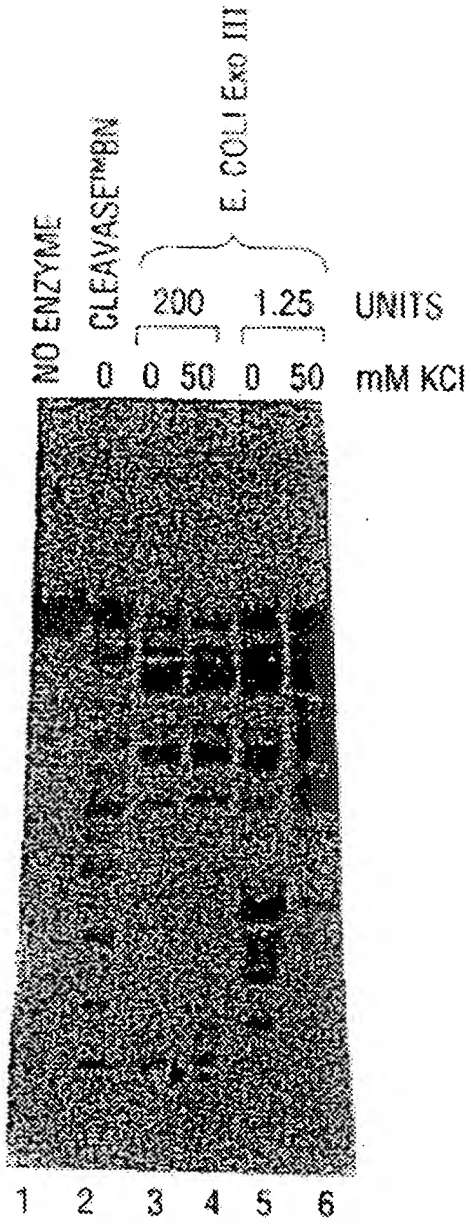

NO ENZYME
CLEAVASE™BN
E. COLI Exo III
200
1.25
UNITS
0 0 50 0 50 mM KCl
1 2 3 4 5 6

FIG. 69

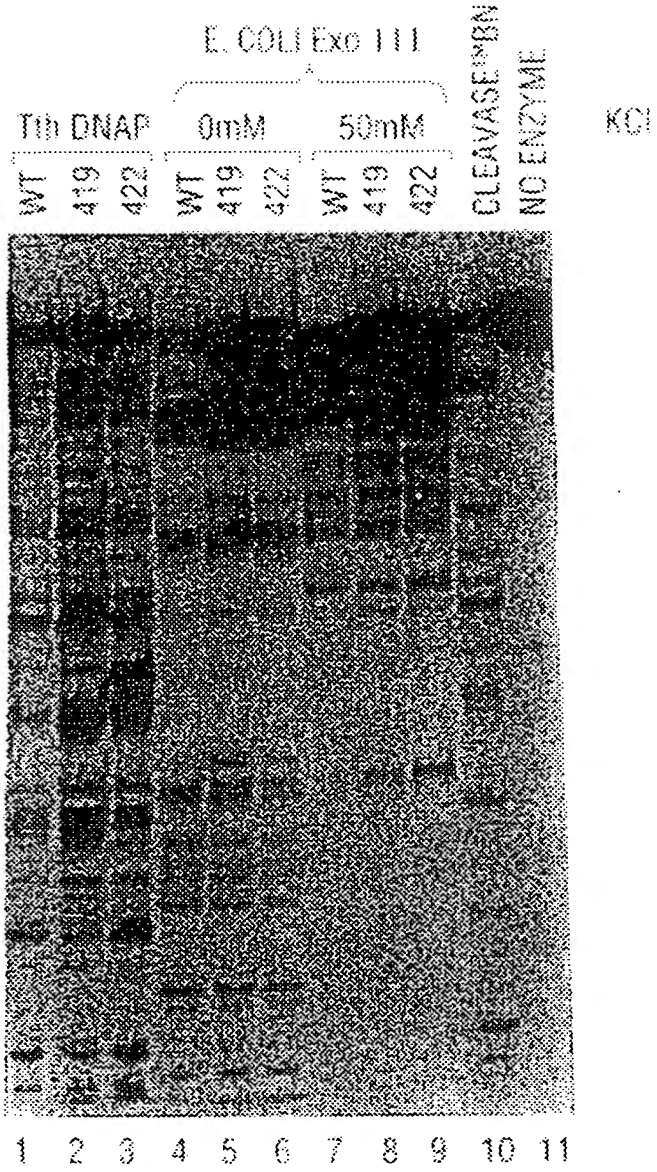

E. COLI Exo III
Tth DNAP
0mM
50mM
KCl
WT
419
422
WT
419
422
WT
419
422
CLEAVASE BN
NO ENZYME
1 2 3 4 5 6 7 8 9 10 11

FIG. 70

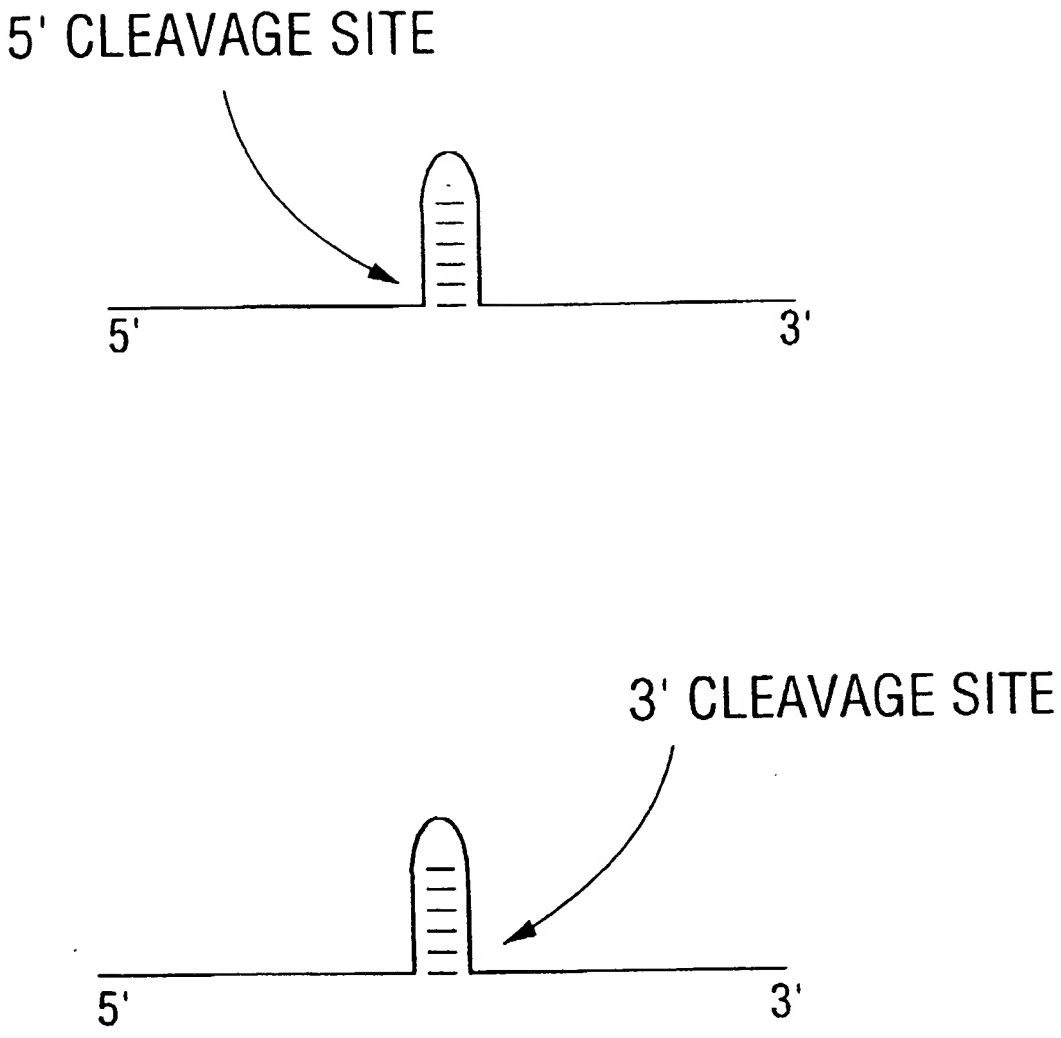


FIG. 71

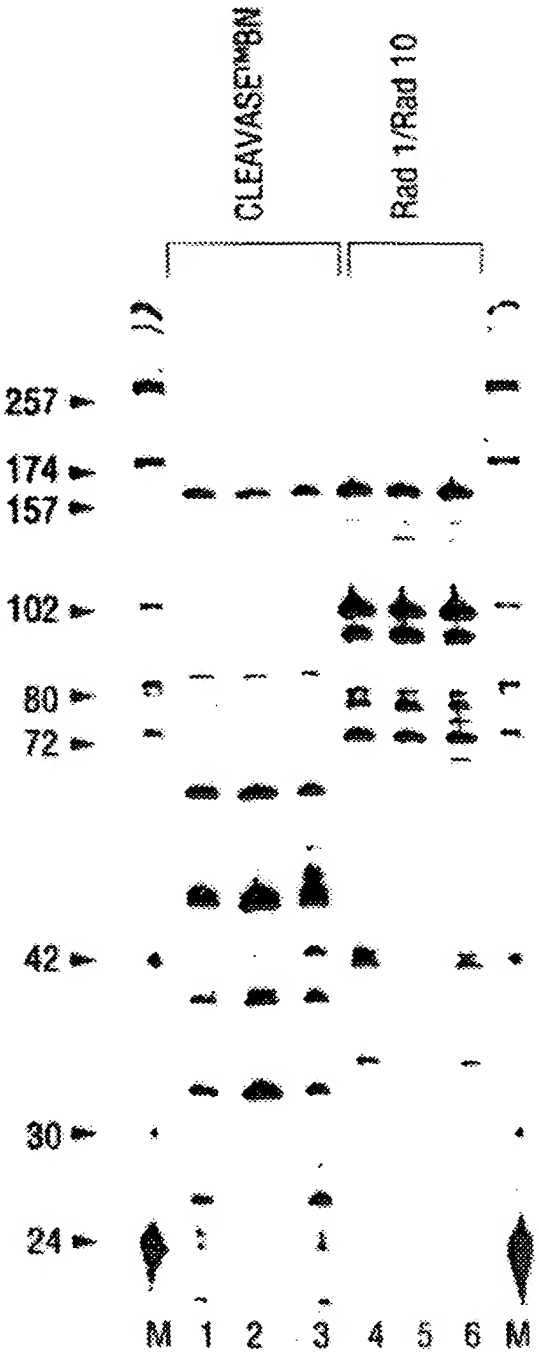


FIG. 72

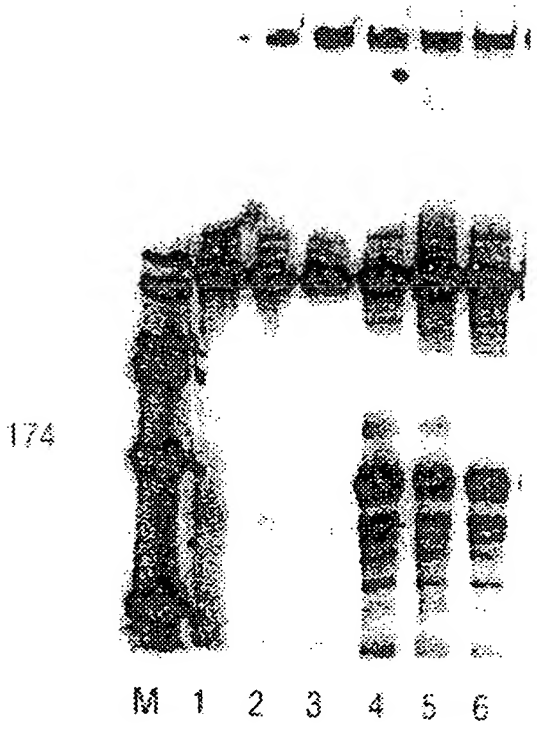


FIG. 73

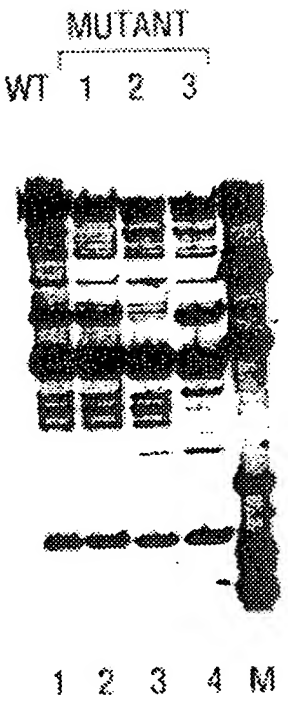


FIG. 74A

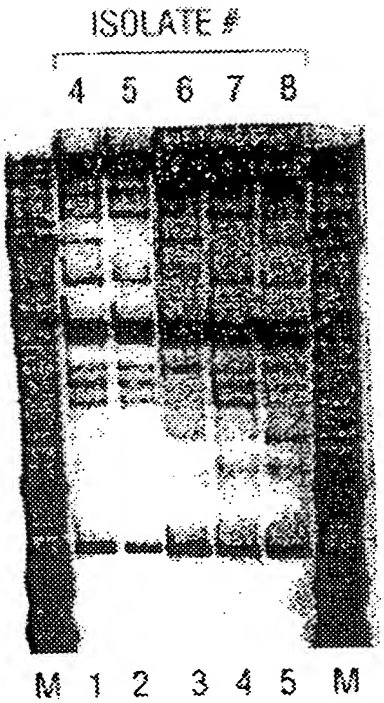


FIG. 74B

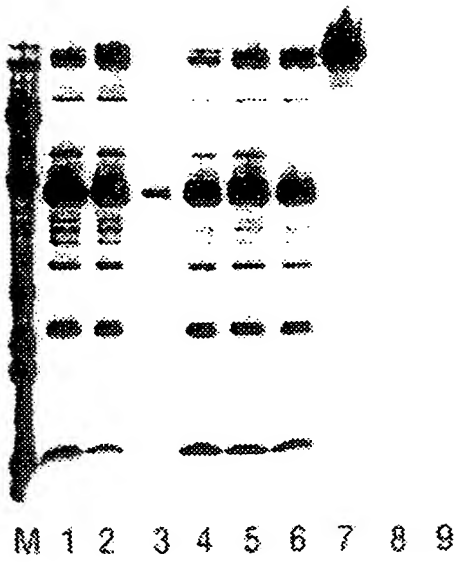


FIG. 75

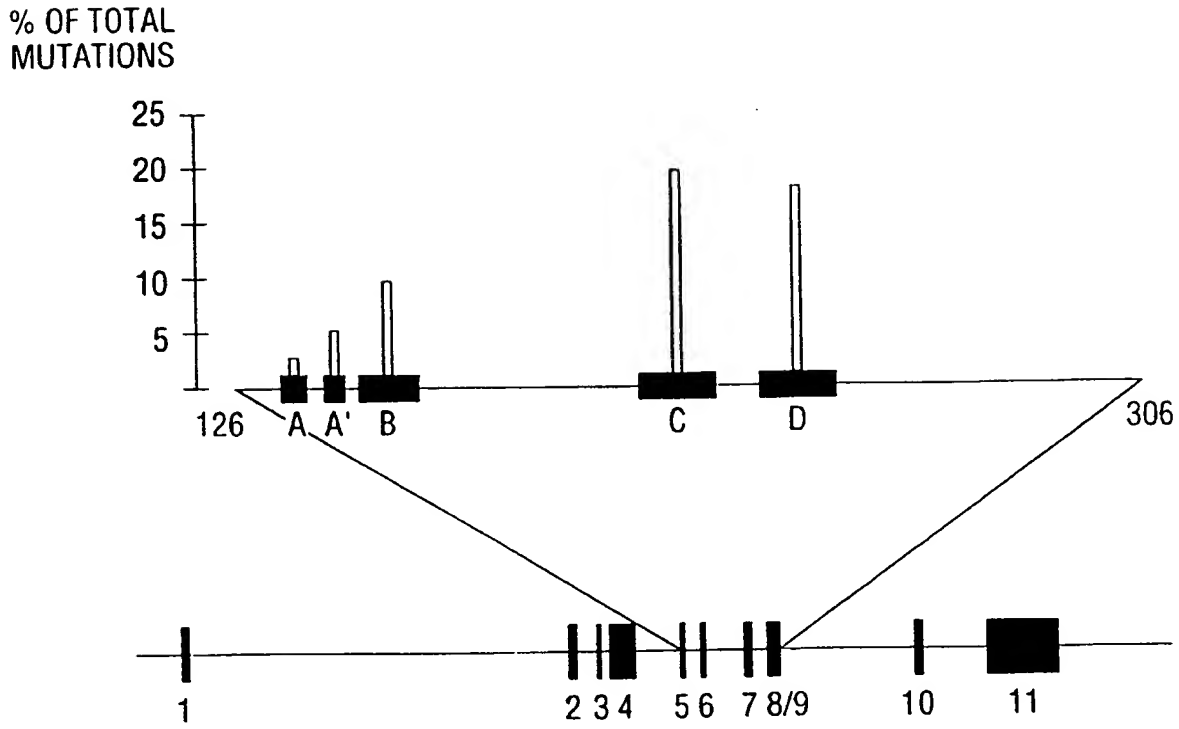


FIG. 76

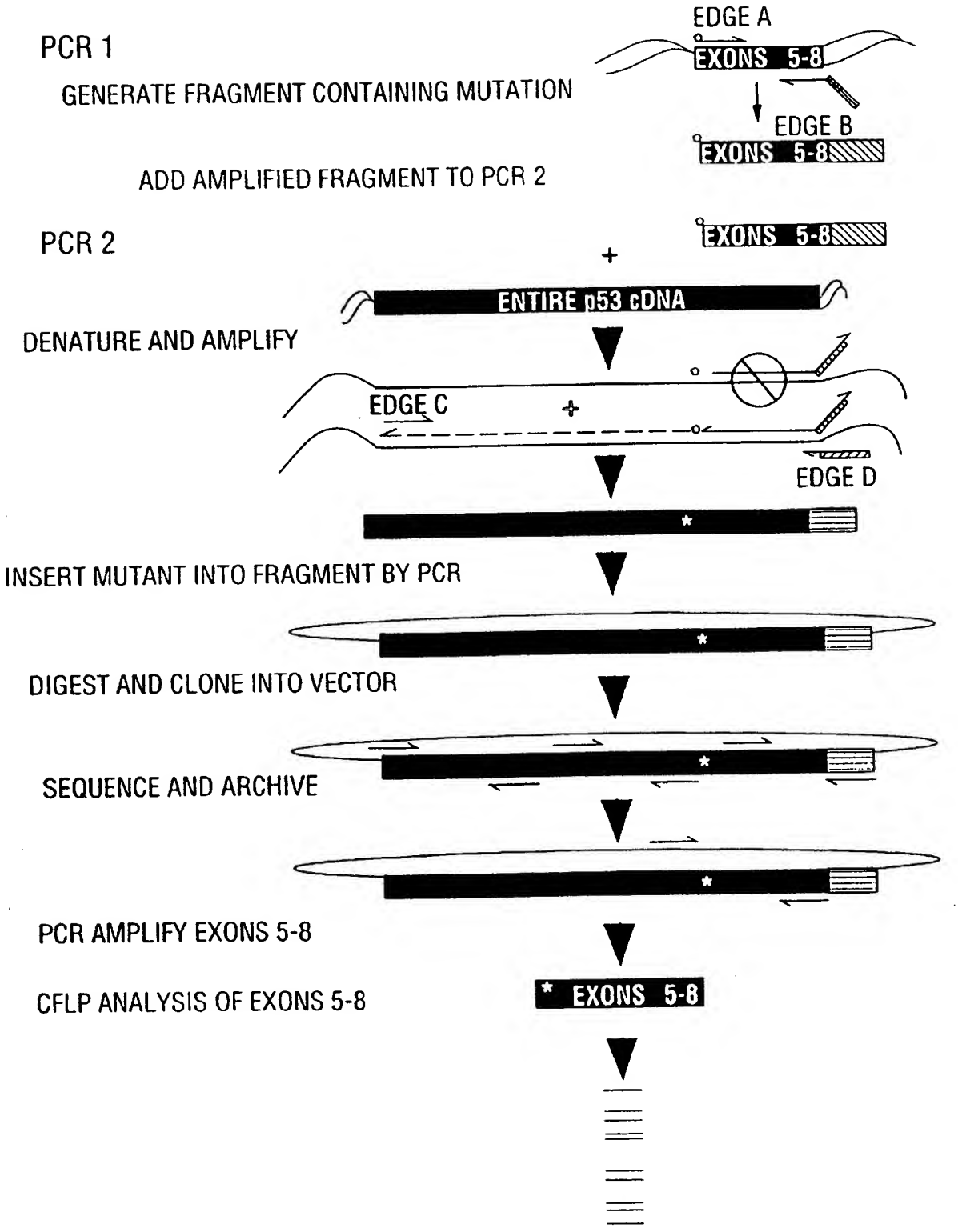

PCR 1
GENERATE FRAGMENT CONTAINING MUTATION
EDGE A
EXONS 5-8
EDGE B
EXONS 5-8
ADD AMPLIFIED FRAGMENT TO PCR 2
PCR 2
EXONS 5-8
+
ENTIRE p53 cDNA
DENATURE AND AMPLIFY
EDGE C
EDGE D
INSERT MUTANT INTO FRAGMENT BY PCR
DIGEST AND CLONE INTO VECTOR
SEQUENCE AND ARCHIVE
PCR AMPLIFY EXONS 5-8
CFLP ANALYSIS OF EXONS 5-8
* EXONS 5-8

FIG. 77

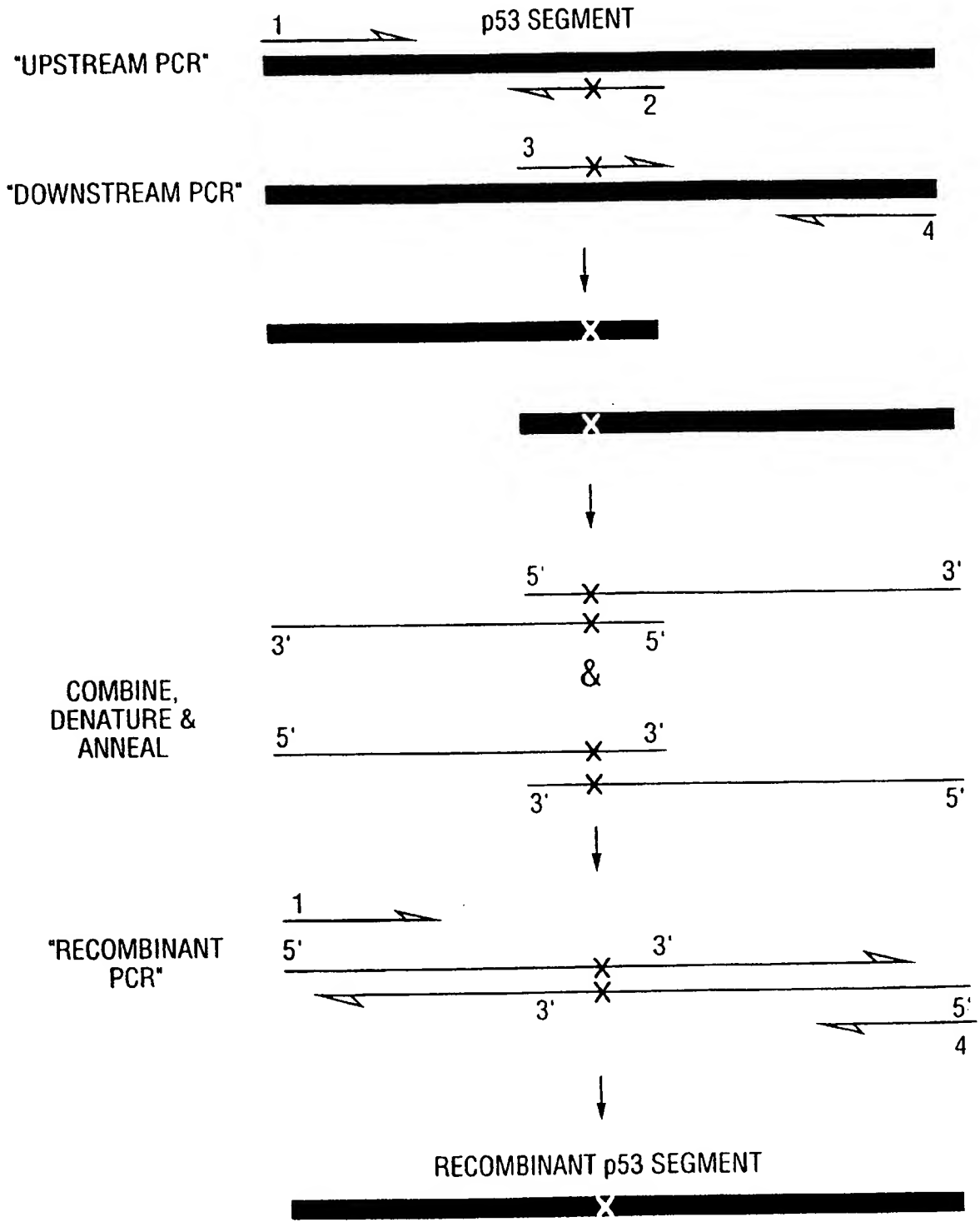

1
p53 SEGMENT
"UPSTREAM PCR"
2
3
"DOWNSTREAM PCR"
4
5'
3'
3'
5'
&
COMBINE,
DENATURE &
ANNEAL
5'
3'
3'
5'
1
"RECOMBINANT
PCR"
5'
3'
3'
5'
4
RECOMBINANT p53 SEGMENT

FIG. 78

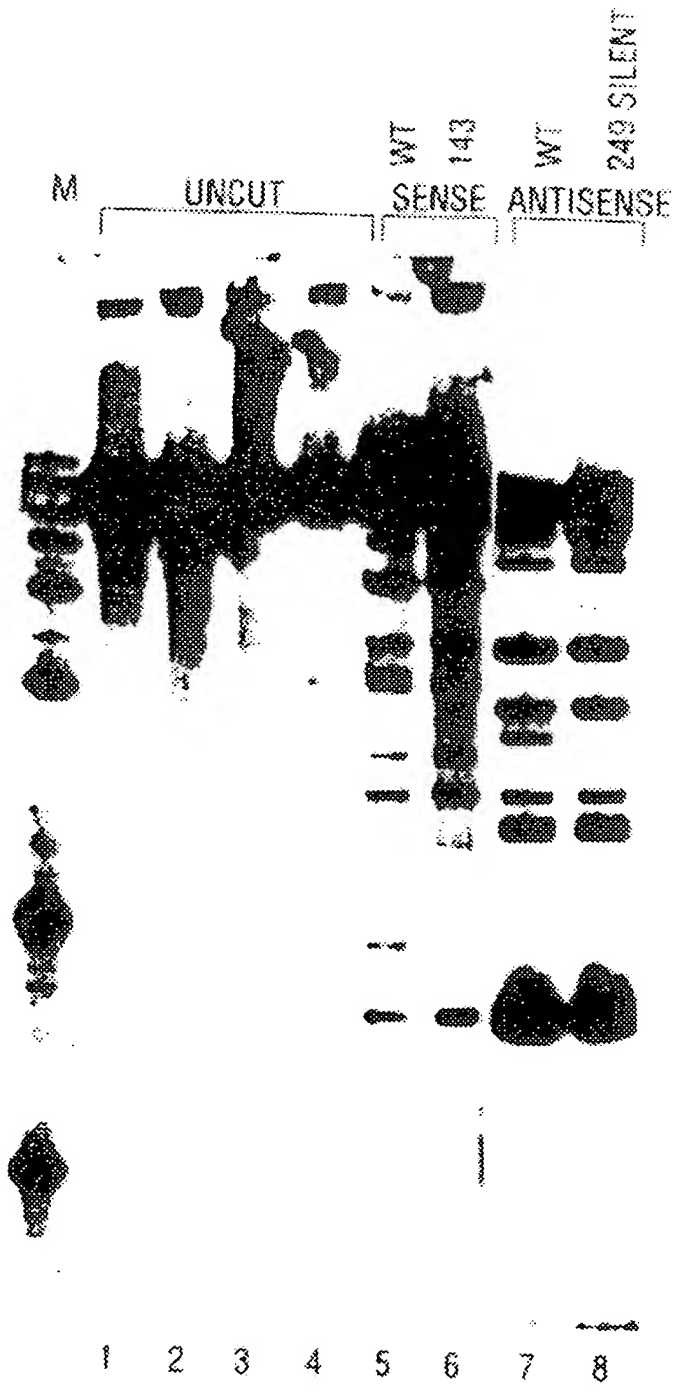


FIG. 79

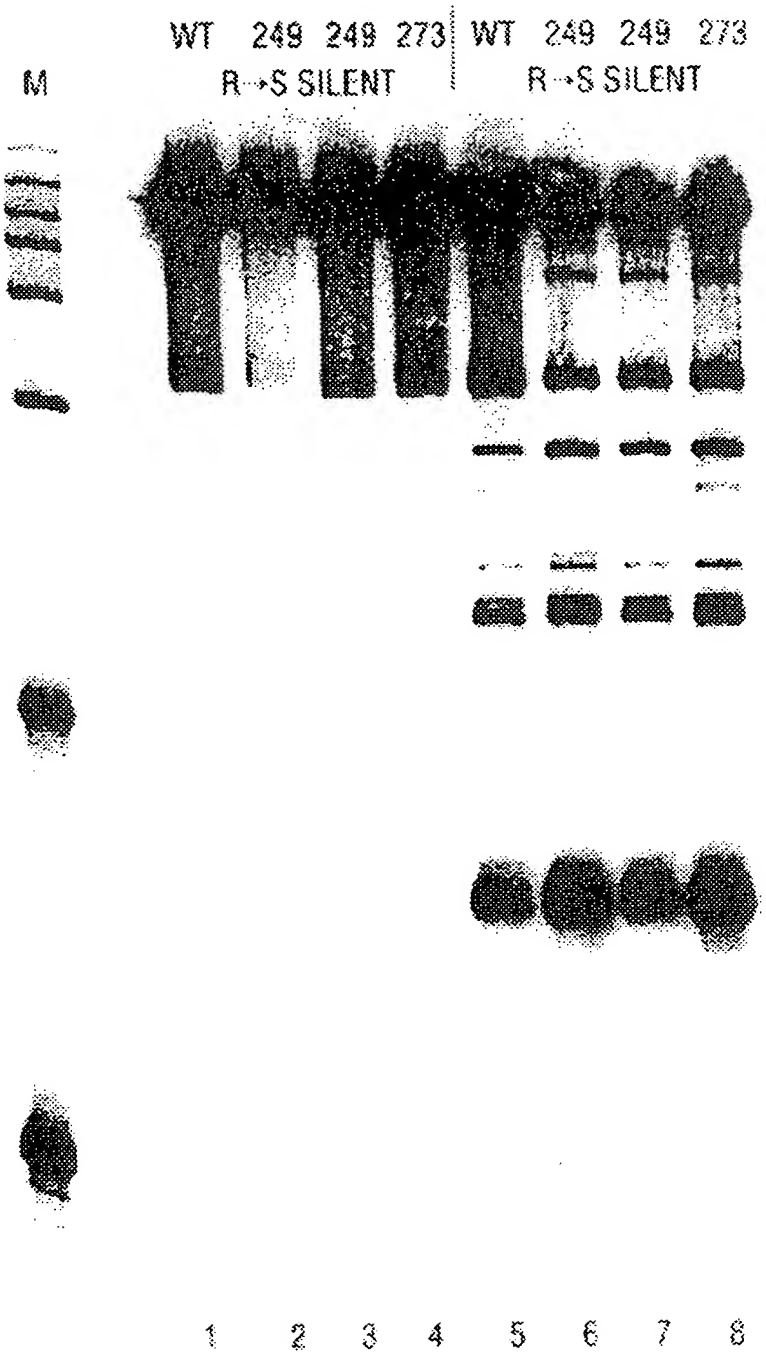


FIG. 80

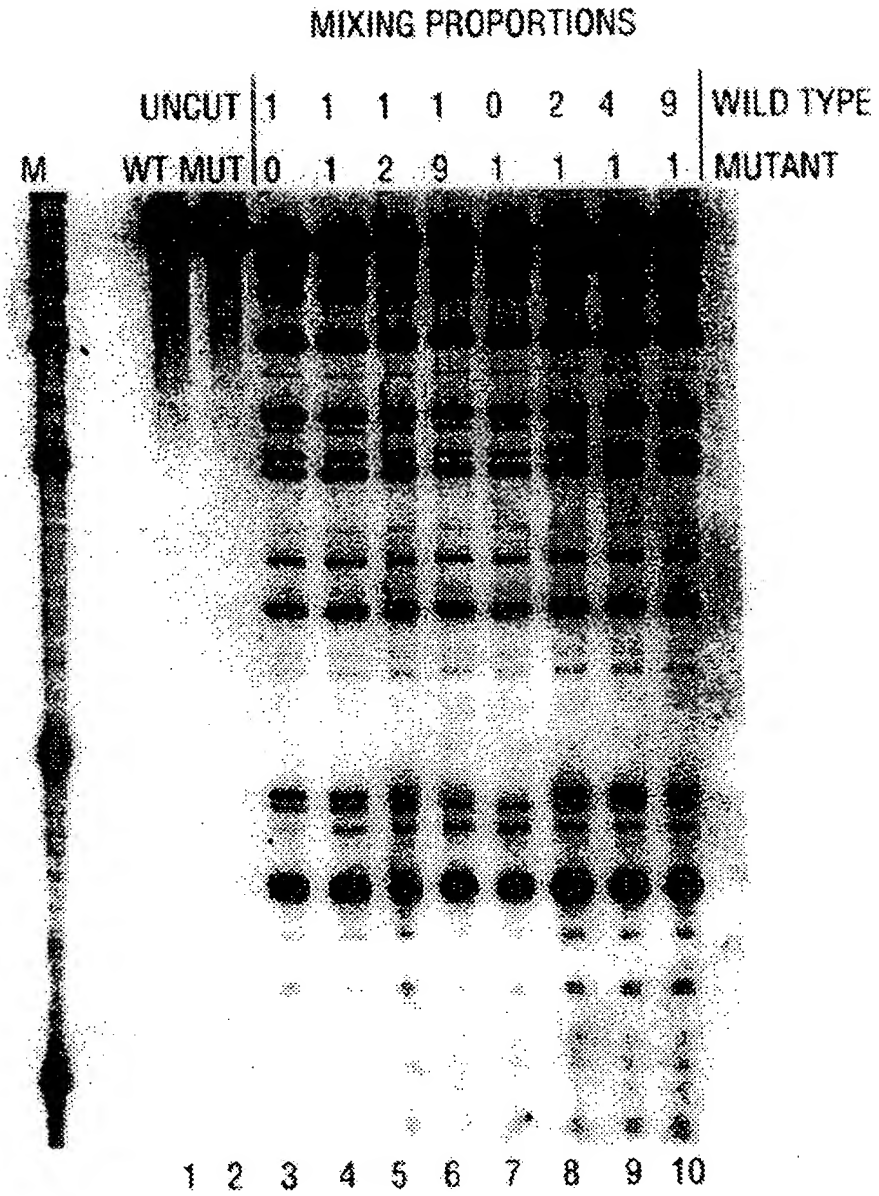

MIXING PROPORTIONS
UNCUT
WT MUT
M
1 1 1 1 0 2 4 9
0 1 2 9 1 1 1 1
WILD TYPE
MUTANT
1 2 3 4 5 6 7 8 9 10

FIG. 81

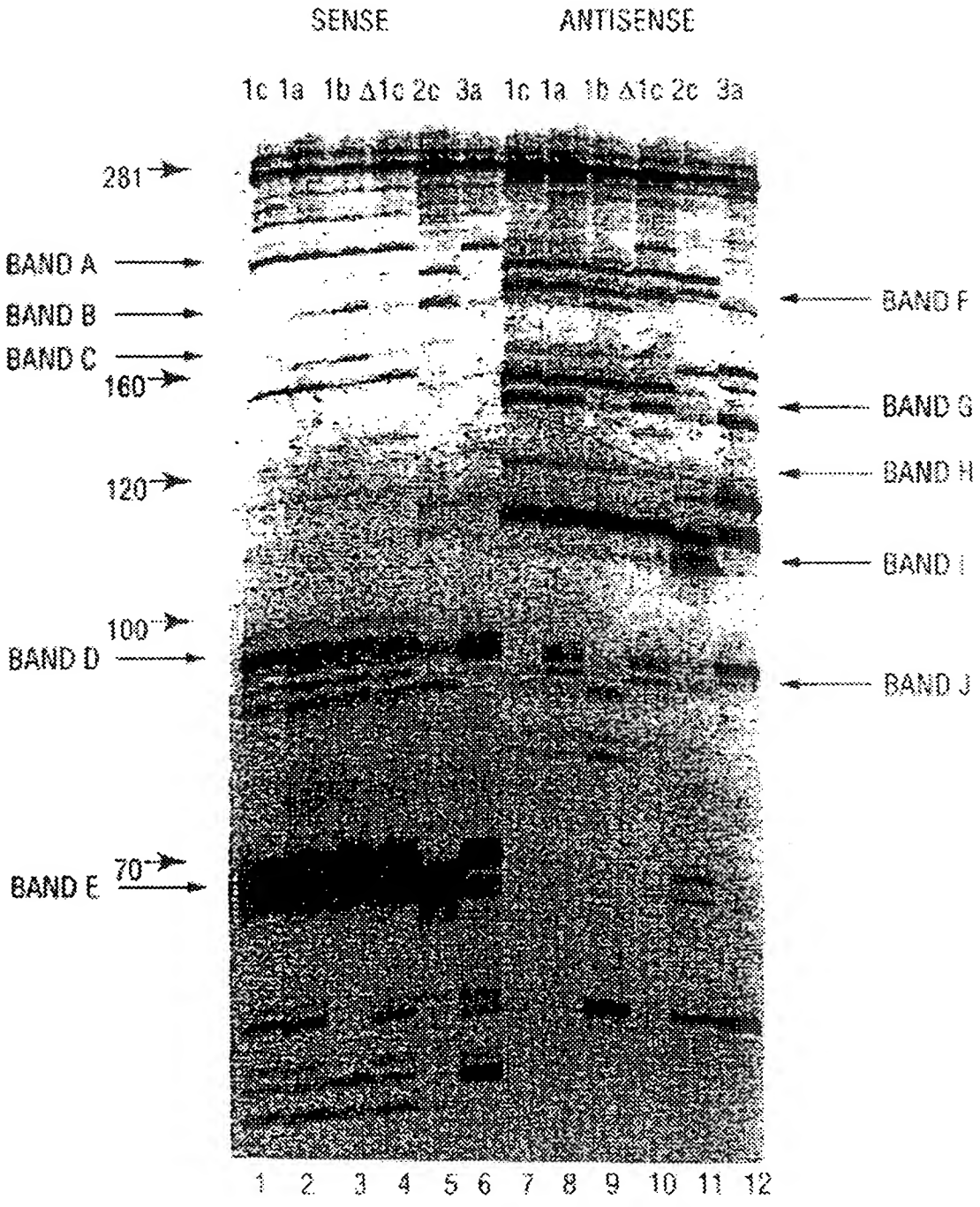

SENSE
ANTISENSE
1c 1a 1b Δ1c 2c 3a 1c 1a 1b Δ1c 2c 3a
281
BAND A
BAND B
BAND C
160
120
100
BAND D
70
BAND E
BAND F
BAND G
BAND H
BAND I
BAND J
1 2 3 4 5 6 7 8 9 10 11 12

FIG. 83

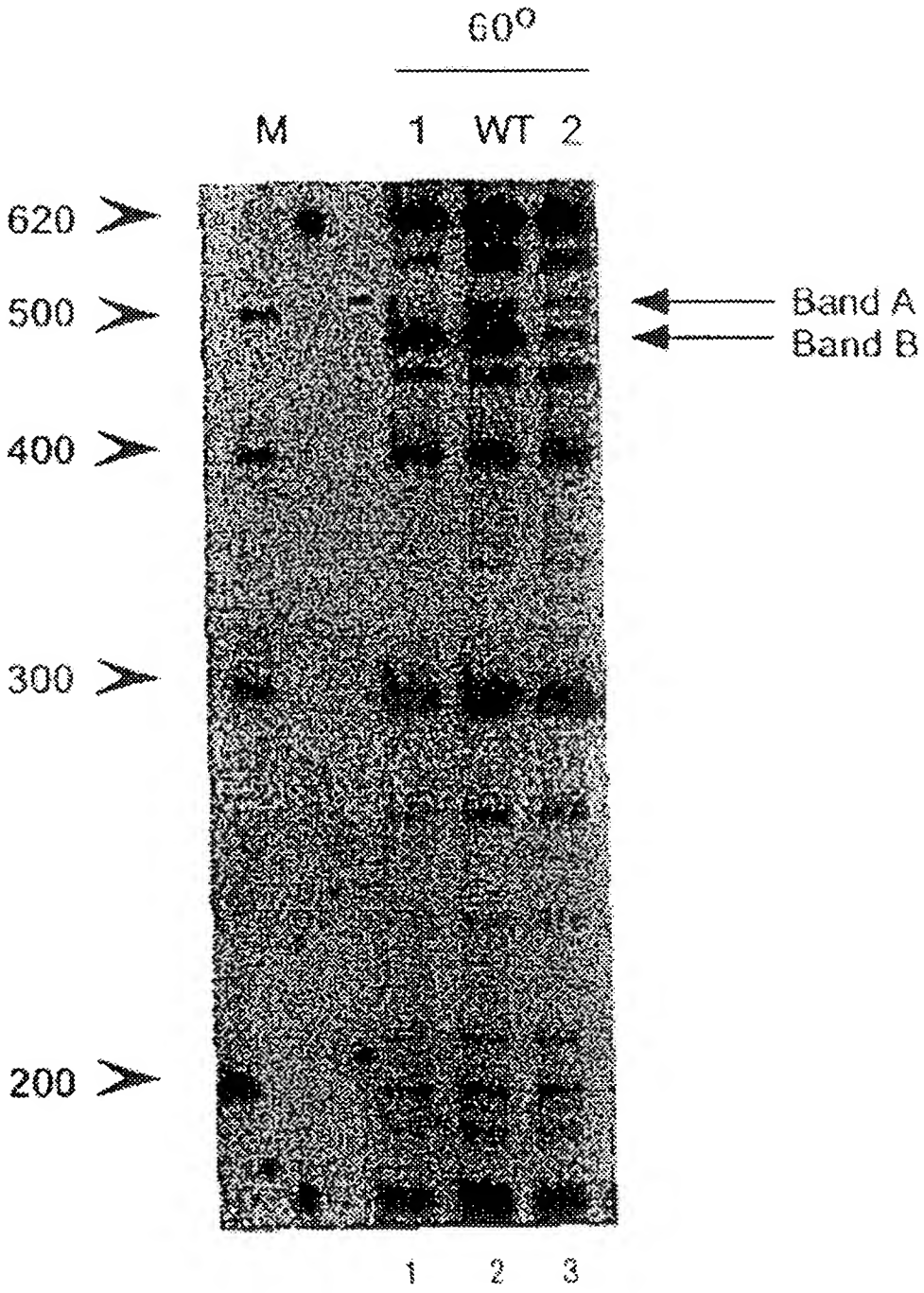


FIG. 84

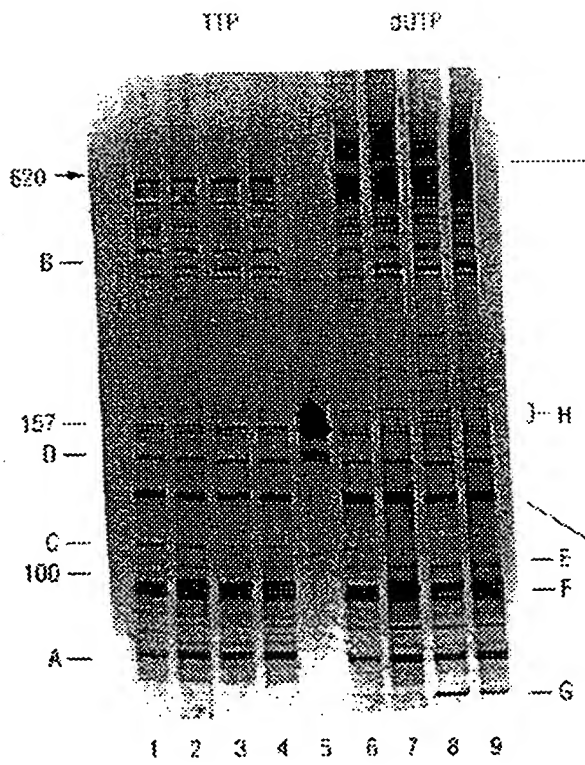


FIG. 85A

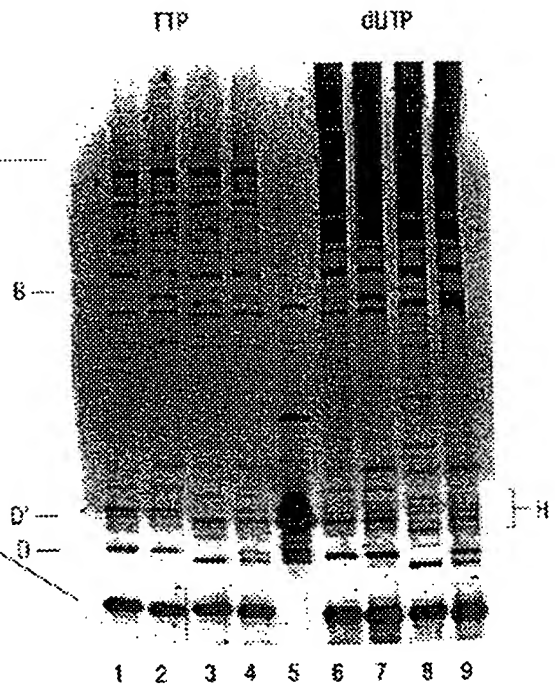


FIG. 85B

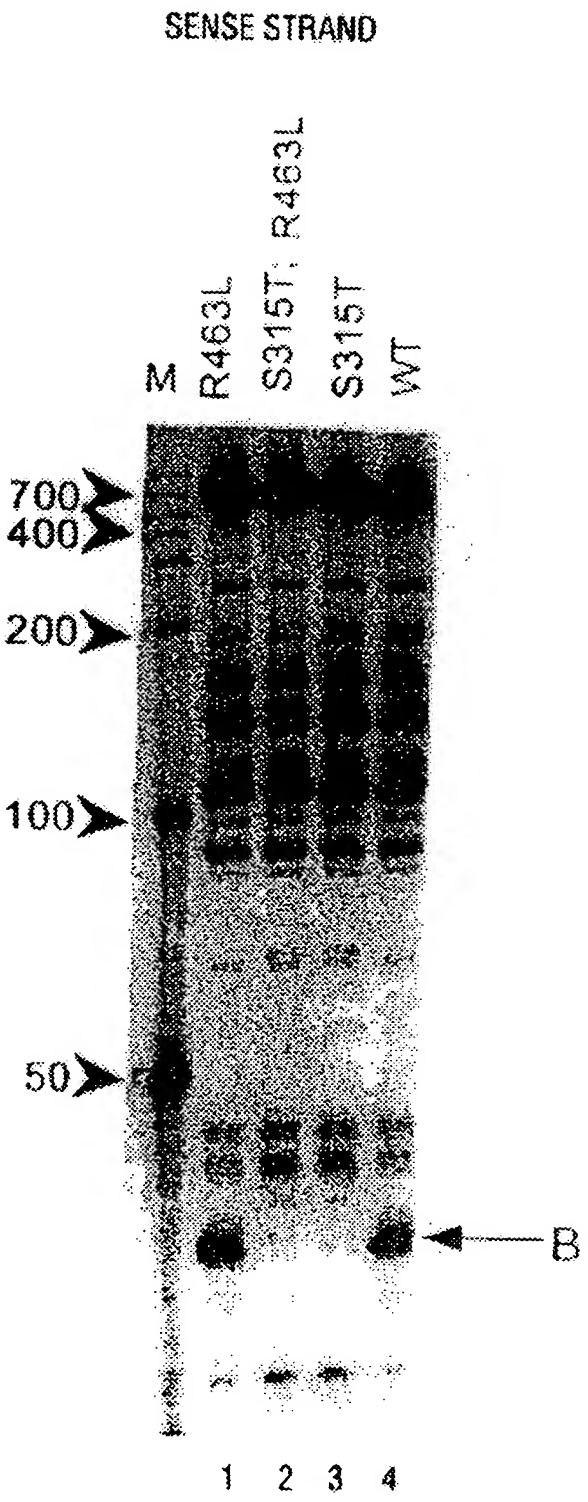

SENSE STRAND
M
R463L
S315T, R463L
S315T
WT
700
400
200
100
50
B
1
2
3
4

FIG. 86

```
HCVI.1 (SEQ ID NO:121)    1 CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG 50
HCV2.1 (SEQ ID NO:122)      CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG
HCV3.1 (SEQ ID NO:123)      CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG
HCV4.2 (SEQ ID NO:124)      CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG
HCV6.1 (SEQ ID NO:125)      CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTA
HCV7.1 (SEQ ID NO:126)      CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCGTG

HCV1.1                     51 CAGCCTCCAG GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC 100
HCV2.1                        CAGCCTCCAG GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC
HCV3.1                        CAGCCTCCAG GICCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC
HCV4.2                        CAGCCTCCAG GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC
HCV6.1                        CAGCCTCCAG GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC
HCV7.1                        CAGCCTCCAG GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC

HCV1.1                    101 GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-AAA 150
HCV2.1                        GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-CAA
HCV3.1                        GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-CAA
HCV4.2                        GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC GTGGATGTAA
HCV6.1                        GGTGAGTACA CCGGAATTGC CGGGAAGACT GGGTCCTTTC TTGGAT-AAA
HCV7.1                        GGTGAGTACA CCGGAATCGC TGGGGTGACC GGGTCCTTTC TTGGAG-CAA
```

FIG. 82A

```
HCV1.1          151 CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCCGCAAGA CTGCTAGCCG 200
HCV2.1              CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCCGCAAGA CTGCTAGCCG
HCV3.1              CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCCGCGAGA CTGCTAGCCG
HCV4.2              CCCGCTCAAT GCCTGGAGAT TTGGGCGTGC CCCCGCAAGA CTGCTAGCCG
HCV6.1              CCCACTCIAT GCCCGGCCAT TTGGGCGTGC CCCCGCAAGA CTGCTAGCCG
HCV7.1              CCCGCTCAAT ACCCAGAAAT TTGGGCGTGC CCCCGCGAGA ICACTAGCCG

HCVI.1          201 AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCCT 250
HCV2.1              AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT
HCV3.1              AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT
HCV4.2              AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT
HCV6.1              AGTAGCGTTG GGTIGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT
HCV7.1              AGTAGTGTTG GGTCGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT

HCVI.1          251 GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC 282
HCV2.1              GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC
HCV3.1              GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC
HCV4.2              GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC
HCV6.1              GCGAGTACCC CGGGAGGTCT CGTAGACCGT GC
HCV7.1              GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC
```

FIG. 82B

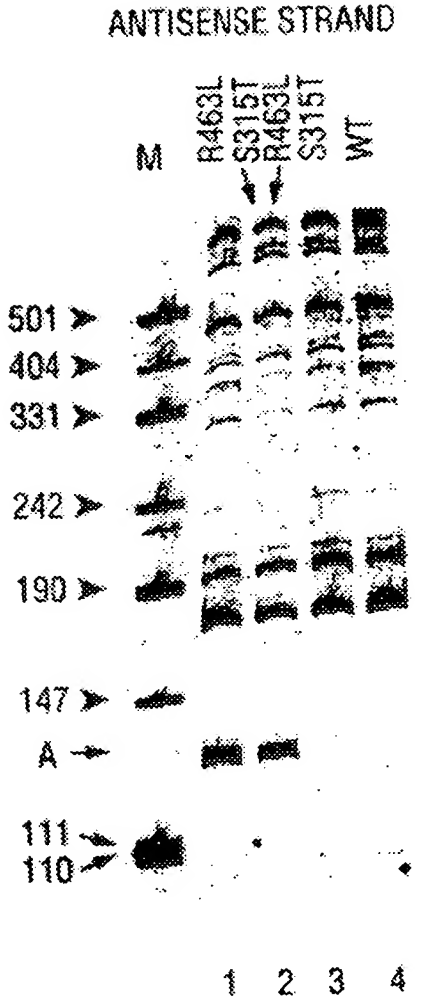

ANTISENSE STRAND
M
R463L
S315T
R463L
S315T
WT
501
404
331
242
190
147
A
111
110
1
2
3
4

FIG. 87

```
          10         20         30         40         50         60
       AGA GTTTGATCCT GGCTCAG                                                  1638
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA
TTTAACTTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

          70         80         90        100        110        120
                                               GGCGGAC GGGTGAGTAA              ER10
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCATT

         130        140        150        160        170        180
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA

         190        200        210        220        230        240
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGGAGAAC GGTAGCCTAC ACGGGTCTAC

         250        260        270        280        290        300
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT

         310        320        330        340        350        360
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCACC
                                       TGA GGATGCCCTC CGTCGTC                  1659
```

FIG. 88A

```
       370        380        390        400        410        420
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT
CCTTATAACG TGTTACCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCTTCCGGA

       430        440        450        460        470        480
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT
AGCCCAACAT TTCATGAAAG TCGCCCCTCC TTCCCTCATT TCAATTATGG AAACGAGTAA

       490        500        510        520        530        540
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG
CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC

       550        560        570        580        590        600
GGTGCAAGCG TTAATCGGAA TTACTGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA
CCACGTTCGC AATTAGCCTT AATGACCCGC ATTTCGCGTG CGTCCGCCAA ACAATTCAGT

       610        620        630        640        650        660
GATGTGAAAT CCCCGGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC
CTACACTTTA GGGGCCCGAG TTGGACCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG

       670        680        690        700        710        720
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTC GAGGAATACC
CATCTCCCCC CATCTTAAGG TCCACATCGC CACTTTACGC ATCTCTAGAC CTCCTTATGG

       730        740        750        760        770        780
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA
CCACCGCTTC CGCCGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTTCG CACCCCTCGT
```

FIG. 88B

```
       790        800        810        820        830        840
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC
TTGTCCTAAT CTATGGGACC ATCAGGTGCG GCATTTGCTA CAGCTGAACC TCCAACACGG

       850        860        870        880        890        900
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA
GAACTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAGCTGG CGGACCCCTC ATGCCGGCGT

       910        920        930        940        950        960
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT
TCCAATTTTG AGTTTACTTA ACTGCCCCCG GGCGTGTTCG CCACCTCGTA CACCAAATTA

       970        980        990       1000       1010       1020
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG
AGCTACGTTG CGCTTCTTGG AATGGACCAG AACTGTAGGT GCCTTCAAAA GTCTCTACTC

      1030       1040       1050       1060       1070       1080
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA
TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAACACT

      1090       1100       1110       1120       1130       1140
                   GC AACGAGCGCA ACCC                                         SB-1

AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC
TTACAACCCA ATTCAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCCG

      1150       1160       1170       1180       1190       1200
                                                   ATG ACGTCAAGTC     SB-3
                                                   ATG ACGTCAAGTC     SB-4
CGGGAACTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC
GCCCTTGAGT TTCCTCTGAC GGTCACTATT TGACCTCCTT CCACCCCTAC TGCAGTTCAG
```

FIG. 88C

```
      1210       1220       1230       1240       1250       1260
ATCATGGCCC TTA                                                          SB-3
ATCATGGCCC TTACGA                                                       SB-4
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG
TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCGC

      1270       1280       1290       1300       1310       1320
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAAC
TGGAGCGCTC TCGTTCGCCT GGAGTATTTC ACGCAGCATC AGGCCTAACC TCAGACGTTG

      1330       1340       1350       1360       1370       1380
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT
AGCTGAGGTA CTTCAGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC CACTTATGCA
                                                    GC CACTTATGCA     1743

      1390       1400       1410       1420       1430       1440
TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT
AGGGCCCGGA ACATGTGTGG CGGGCAGTGT GGTACCCTCA CCCAACGTTT TCTTCATCCA
AGGGCCCGGA ACATG                                                      1743

      1450       1460       1470       1480       1490       1500
AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA
TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTCAGCATT

      1510       1520       1530       1540       1550
CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA........
GTTCCATTGG CATCCCCTTG GACGCCAACC TAGTGGAGGA AT........
```

FIG. 88D

```
1638 (SEQ ID NO:151)                    AGAGTTTGATCCTGGCTCAG
E.colirrsE(SEQ ID NO:158)0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5(SEQ ID NO:159)0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAATACATGCA
Stp.aureus(SEQ ID NO:160)0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCA

ER10 (SEQ ID NO:152)                                                    GGCGGACGGG
E.colirrsE                60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
Cam.jejunS                62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAGTGGA-----TTAGTGGCGCACGGG
Stp.aureus                61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG

ER10                         TGAGTAA
E.colirrsE               114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA
Cam.jejun5               114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGGAAACGACTGCTAATA
Stp.aureus               113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA

E.colirrsE               175 CCGCATAAC-------GTCGCAAGAC--------CAAAGAGGGGGACCTTCG-GGCCTCTTG
Cam.jejun5               176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-GAAAG---------TTTTT-------CG
Stp.aureus               175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirrsE               221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGA
Cam.jejun5               221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
Stp.aureus               229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirrsE               283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
Cam.jejun5               283 CGCTTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA
Stp.aureus               291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
1659(COMPL)                                                             ACTCCTA
```

FIG. 89A

```
E.colirrsE          345 CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
Cam.jejun5          345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAAACCCTGACGCAGCAACGCCGCGTG
Stp.aureus          353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
1659(COMPL)             CGGGAGGCAGCAG

E.colirrsE          407 TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5          407 GAGGATGACACTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAG ----------AATT
Stp.aureus          415 AGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAC

E.colirrsE          468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5          455 C----------TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus          476 -TGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG
```

FIG. 89B

```
E.colirrsE   530 GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5   506 GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGATT
Stp.aureus   538 GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTT

E.colirrsE   592 GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT
Cam.jejun5   568 ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAAACTGCTTGGGAAACTGATAGTCTA
Stp.aureus   600 TTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTT

E.colirrsE   654 GAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5   630 GAGTGAGGGAGAGGCAGATGGAATTGGTGGTGTAGGGGTAAAATCCGTAGATATCACCAAGA
Stp-aureus   662 GAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA

E.colirrsE   716 ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam.jejun5   692 ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus   724 ACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA

E.colirrsE   778 GCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5   754 GCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus   786 TCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG
```

FIG. 89C

```
E.colirrsE   840 C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
Cam.jejun5   816 G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAGTGTACCGCCTGGGGAGTACGGTCGC
Stp.aureus   848 GT-TTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGC

E.colirrsE   900 AAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATT
Cam.jejun5   876 AAGATTAAAACTCAAAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATT
Stp.aureus   909 AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATT

E.colirrsE   962 CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTCAGAGATGAGAAT
Cam.jejun5   938 CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
Stp.aureus   971 CGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC

E.colirrsE  1024 GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGA
Cam.jejun5  1000 GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCGTGTCGTGA
Stp.aureus  1033 TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGA

SB-1                                      GCAACGAGCGCAACCC
E.colirrsE  1081 AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
Cam.jejun5  1061 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG-CC
Stp.aureus  1092 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCA-TTAAGT-T
```

FIG. 89D

```
SB-3 (SEQ ID NO:157)                                                    ATGACGTCAAGTCATC
SB-4 (SEQ ID NO:154)                                                    ATGACGTCAAGTCATC
E.colirrsE   1142 GGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5   1122 GAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus   1152 GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC

SB-3                ATGGCCCTTA
SB-4                ATGGCCCTTACGA
E.colirrsE   1204 ATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTC
Cam.jejun5   1183 ATGGCCCTTATGCCCAGGGCGACACACGTGCTACAATGGCATATAGAATGAGACGCAATACC
Stp.aureus   1214 ATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGACAATACAAAGGGCAGCGAAACC

E.colirrsE   1266 GCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5   1245 GCGAGGTGGAG-CAAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus   1276 GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA

E.colirrsE   1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5   1306 CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus   1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743(compl)                                                             CGGTGAATACGTTCCCGGGC
```

FIG. 89E

```
E.colirrsE      1389 CTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCT
Cam.jejun5      1368 CTTGTACTCACCGCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
Stp.aureus      1399 ATTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCT
1743(compl)          CTTGTAC

E.colirrsE      1451 TCG-GGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5      1427 AC---T-AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus      1461 TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCG

E.colirrsE      1512 TAGGGGAACCTGCGGTTGGATCACCTCCTTA---
Cam.jejun5      1485 TAGGAGAACCTGCGGTTGGATCACCTCCT-----
Stp.aureus      1523 TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-
```

FIG. 89F

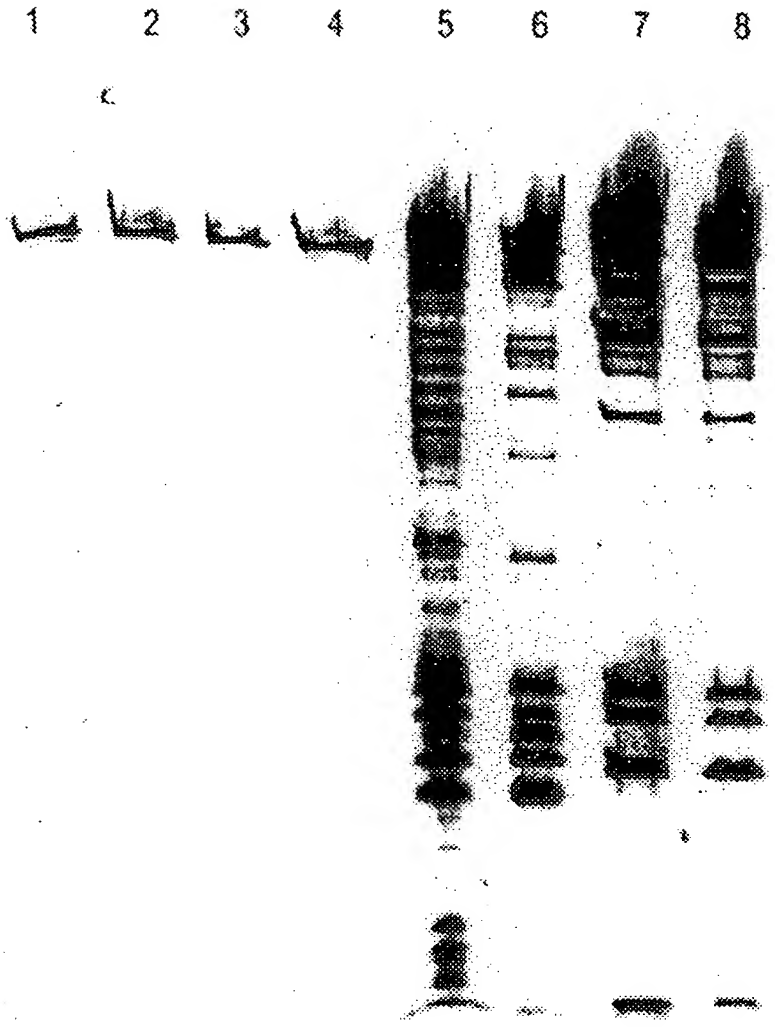


FIG. 90

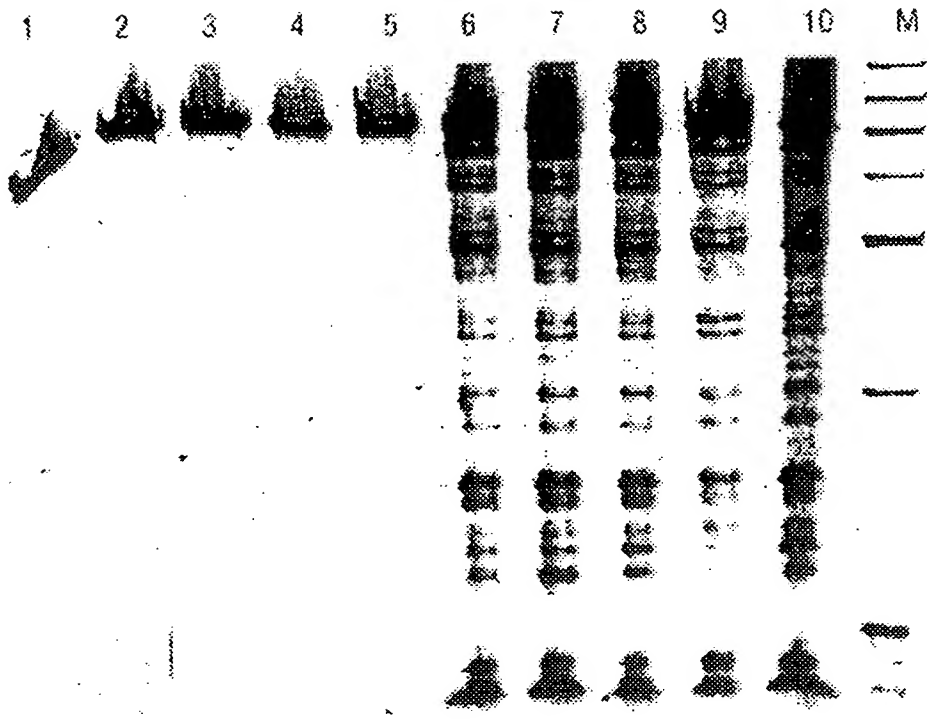


FIG. 91A

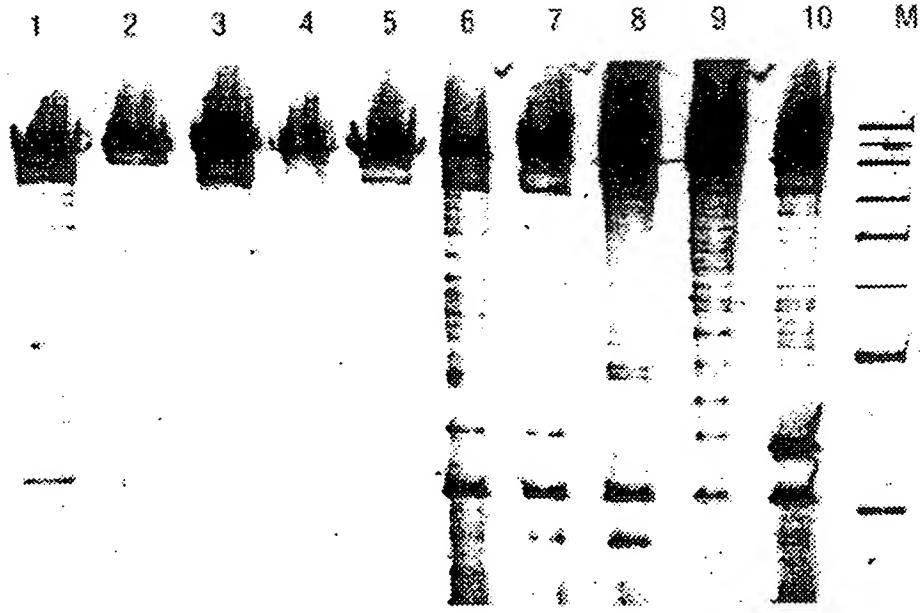


FIG. 91B

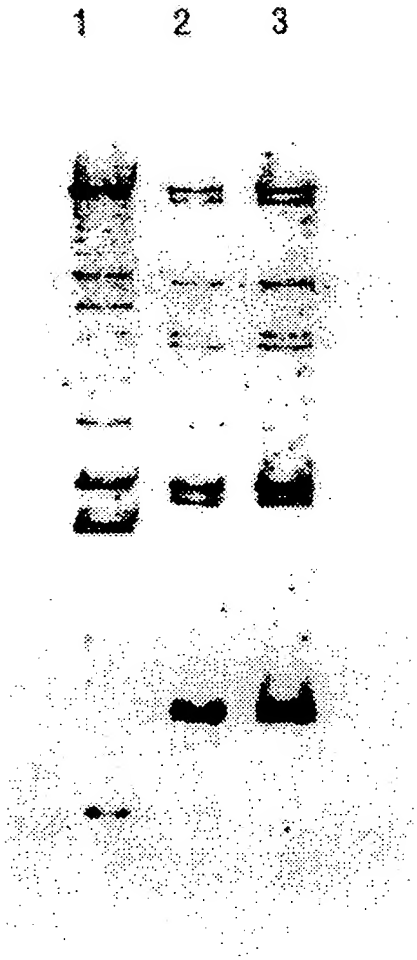


FIG. 92

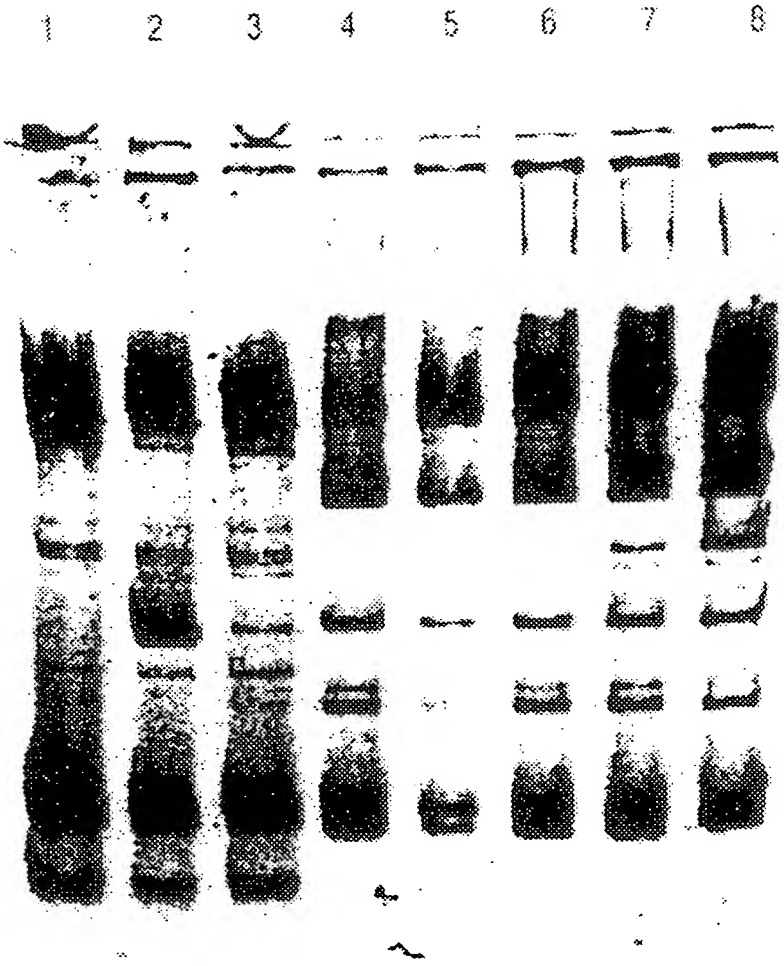


FIG. 93

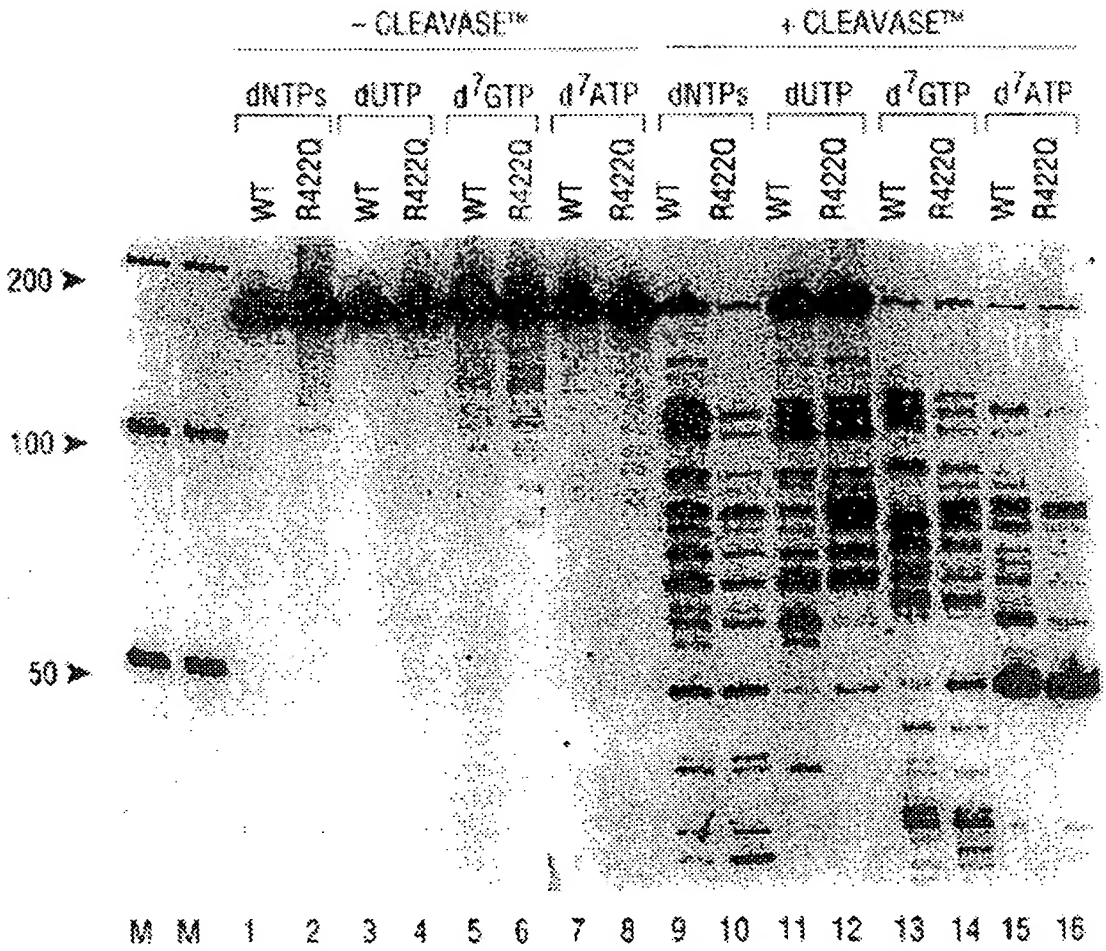

- CLEAVASE™
+ CLEAVASE™
dNTPs
dUTP
d7GTP
d7ATP
WT
R422Q
200
100
50
M M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

FIG. 94